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OM protein - protein search, using sw model

Run on: September 14, 1999, 09:51:02 ; Search time 16.15 Seconds

(without alignments)
1341.385 Million cell updates/sec

Title: US-09-104-063-4

Perfect score: 1830

Sequence: 1 MEGISITSTNNTTEEMSGSD.....KRGHSHSVSTSESSSPFHS 352

Scoring table: BLOSUM62

Searched: 201082 seqs, 61543640 residues

Database: SPTREMBL_10:*

1: sp_archaea:*\n2: sp_bacteria:*\n3: sp_fungi:*\n4: sp_human:*\n5: sp_invertebrate:*\n6: sp_mammal:*\n7: sp_mhc:*\n8: sp_organelle:*\n9: sp_phage:*\n10: sp_plant:*\n11: sp_protist:*\n12: sp_virus:*\n13: sp_vertebrate:*\n14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1816	99.2	360	4	060835	060835 homo sapien
2	1806	98.7	352	6	077488	077488 cercopithec
3	1548.5	84.6	332	11	062973	062973 rattus norv
4	1386	75.7	358	13	0976C3	0976C3 xenopus lae
5	1161	63.4	357	13	042445	042445 oncorhynch
6	1121.5	61.3	353	13	093247	093247 cyprinus ca
7	578	31.6	367	11	088410	088410 mus musculu
8	574.5	31.4	415	4	015185	015185 homo sapien
9	569	31.1	367	11	054689	054689 mus musculu
10	564	30.8	356	6	097571	097571 canis fam11
11	544	29.7	392	13	093281	093281 gallus gall
12	535.5	29.3	378	11	008707	008707 mus musculu
13	528	28.9	356	6	097665	097665 macaca mula
14	526.5	28.8	382	11	009027	009027 rattus norv
15	521.5	28.5	373	11	055193	055193 rattus norv
16	519.5	28.4	383	12	089609	089609 equine herp
17	518.5	28.3	360	6	018793	018793 macaca mula
18	515.5	28.1	352	6	097883	097883 hylobates 1
19	514.5	28.1	384	4	000590	000590 homo sapien
20	512.5	28.0	384	4	000537	000537 homo sapien
21	509	27.8	352	6	097975	097975 macaca arct
22	509	27.8	358	11	092213	092213 cavia porce
23	508	27.8	352	6	018771	018771 pan troglod
24	507	27.7	352	6	097881	097881 pongo pygma
25	507	27.7	352	6	077776	077776 cercocebus
26	507	27.7	352	6	097962	097962 pygathrix a
27	506	27.7	352	4	015538	015538 homo sapien
28	506	27.7	352	6	018772	018772 pan troglod
29	506	27.7	352	6	097878	097878 trachypithe

ALIGNMENTS

30	506	27.7	352	6	097879	097879 trachypithe
31	506	27.7	352	6	097880	097880 pygathrix b
32	505	27.6	352	6	018770	018770 pan troglod
33	505	27.6	352	6	097882	097882 pygathrix n
34	504	27.5	354	11	0920D9	0920D9 mus musculu
35	498	27.2	368	13	042444	042444 oncorhynch
36	496	27.1	334	6	097724	097724 felis silve
37	495.5	27.1	372	13	093237	093237 cyprinus ca
38	495.5	27.1	342	13	093239	093239 cyprinus ca
39	487	26.6	344	6	077833	077833 cercocebus
40	482	26.3	351	6	097774	097774 felis silve
41	468.5	25.6	362	11	089039	089039 rattus norv
42	465	25.4	359	11	054814	054814 rattus norv
43	454.5	24.8	333	4	014694	014694 homo sapien
44	426	23.3	353	13	P79960	P79960 xenopus lae
45	409	22.3	351	11	088536	088536 mus musculu

RESULT 1	PRELIMINARY;	PRT;	360 AA.
060835			
ID 060835:			
AC 060835:			
DT 01-AUG-1998 (TREMBlrel. 07, Created)			
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)			
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)			
DE CXCR4 GENE ENCODING RECEPTOR CXCR4.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;			
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
RP [1]			
RA MEDLINE; 98258970.			
RA CARUT A., SAMSOM M., ALONSO J.M., ALCAMI J., BALPUS F.,			
RA VIRELIZIER J.L., PARMENTIER M., AREZANA-SEISEDOS F.,			
RA "genomic organization and promoter characterization of human CXCR4			
RT gene."			
RL FEBS Lett. 426:271-278(1998).			
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).			
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
DR EMBL; AJ224699; CAA12166.1; -.			
DR PIRAM; PF00001; 7tm.1; 1.			
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.			
KW G-protein coupled receptor; Transmembrane; Glycoprotein.			
SO SEQUENCE 360 AA; 40607 MW; 110EB9E6 CRC32;			
Query Match	99.28;	Score 1816;	DB 4; Length 360;
Best Local Similarity	97.88;	Pred. No. 2.3e-138;	
Matches 352; Conservative	0;	Mismatches 0;	Indels 8; Gaps 1;
QY 1	MEGIS-----TSTNTTEEMSGSDYDSMKPCREENANFNKIFLPITYSIIFLTG 52		
Db 1	MEGISSTPLPLDQYITSDNTTEEMSGSDYDSMKPCREENANFNKIFLPITYSIIFLTG 60		
QY 53	IVNGVILVWGQYQKRLRSMTDKYRLHLSVADLLFVTLPEWADAVANWYGFNLCKAV 112		
Db 61	IVNGVILVWGQYQKRLRSMTDKYRLHLSVADLLFVTLPEWADAVANWYGFNLCKAV 120		
QY 113	HVITVNVYSVLLAFISIDRYLAIVHANSQPRKLEKVVYGVWTPALLTTPDF 172		
Db 121	HVITVNVYSVLLAFISIDRYLAIVHANSQPRKLEKVVYGVWTPALLTTPDF 180		
QY 173	IFANVSEADRYICDREYPNDLWVVPFOHIMVGLIPGIVILSCYCIISKLSHSGH 232		
Db 181	IFANVSEADRYICDREYPNDLWVVPFOHIMVGLIPGIVILSCYCIISKLSHSGH 240		
QY 233	OKRAKATTVILILAFACWLPYIGISIDSFILLEIKGCGCEPENTVHKWISTELAF 292		
Db 241	OKRAKATTVILILAFACWLPYIGISIDSFILLEIKGCGCEPENTVHKWISTELAF 300		

OY 293 FHCCINPIYAFGAKFKTSAQHATLSVSRGSSKILSKRGHSSVTESSSFHSS 352
 DB 301 FHCCINPIYAFGAKFKTSAQHATLSVSRGSSKILSKRGHSSVTESSSFHSS 360

RESULT 2
 077488 PRELIMINARY: PRT: 352 AA.

ID 077488
 AC 077488. PRELIMINARY: PRT: 352 AA.
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-MAY-1999 (TREMBlrel. 08, Last sequence update)
 DE CXC4 RECEPTOR.
 OS Cercopithecus aethiops (Green monkey) (Givet).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae;
 OC Chlorocebus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MURAYAMA Y., MATSUNAGA S., INOUE-MURAYAMA M.;
 RT "cDNA sequence of African green monkey CXCR-4 chemokine receptor
 gene."
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AB015943; BAA31327.1; -.
 DR PFAM: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G-PROTEIN_RECEPTOR; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 SQ SEQUENCE 352 AA; 39773 MW; BD6D5150 CRC32;

Query Match 98.7%; Score 1806; DB 6; Length 352;
 Best Local Similarity 98.6%; Pred. No. 1.4e-137;
 Matches 347; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 MEGISITSDNTYEMSGDYSKMKPCFRENANFKIFLPTIYSIIFLTGIVNGLYI 60
 DB 1 MEGISITSDNTYEMSGDYSKMKPCFRENANFKIFLPTIYSIIFLTGIVNGLYI 60
 OY 61 LVMGYQKLRMTDKYRLHLVSADLLFVITLPFWAVDAVANWFGNLCRAVHYITVNL 120
 DB 61 LVMGYQKLRMTDKYRLHLVSADLLFVITLPFWAVDAVANWFGNLCRAVHYITVNL 120
 OY 121 YSSVLLIATISIDRYLATYHATNSQPRKLLAEKVVYVGVWIPALLITPDIPIANVSEA 180
 DB 121 YSSVLLIATISIDRYLATYHATNSQPRKLLAEKVVYVGVWIPALLITPDIPIANVSEA 180
 OY 181 DORYICDRYPNDLWVVFQFQIHMGILPGIYLSCYIIISKLSHSGHQKRAKLT 240
 DB 181 DORYICDRYPNDLWVVFQFQIHMGILPGIYLSCYIIISKLSHSGHQKRAKLT 240
 OY 241 TVILLAFACWLPYYIGISIDSIFILEITIKGCEPENTVHKWISTEALAFHCCLANPI 300
 DB 241 TVILLAFACWLPYYIGISIDSIFILEITIKGCEPENTVHKWISTEALAFHCCLANPI 300
 OY 301 LYAFGAKFKTSAQHATLSVSRGSSKILSKRGHSSVTESSSFHSS 352
 DB 301 LYAFGAKFKTSAQHATLSVSRGSSKILSKRGHSSVTESSSFHSS 352

RESULT 3
 062973 PRELIMINARY: PRT: 332 AA.

ID 062973
 AC 062973.
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-MAY-1999 (TREMBlrel. 01, Last sequence update)
 DE CHEMOKINE RECEPTOR LCRI.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RA WONG M., XIN W.W., DUMAN R.S.;
 RL Mol. Psych. 0:0-0(0).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: U54791; AAB01981.1; -.
 DR PFAM: PF00001; 7tm_1; 2.
 DR PROSITE: PS00237; G-PROTEIN_RECEPTOR; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 SQ SEQUENCE 332 AA; 37442 MW; C0EAB84B CRC32;

Query Match 84.6%; Score 1548.5; DB 11; Length 332;
 Best Local Similarity 86.0%; Pred. No. 6.1e-117;
 Matches 300; Conservative 16; Mismatches 16; Indels 17; Gaps 2;

OY 4 ISITYSDNYTEEMSGDYSKMKPCFRENANFKIFLPTIYSIIFLTGIVNGLYI 63
 DB 1 MEITYSDNYSEVGSGDYSKMKPCFRENANFKIFLPTIYSIIFLTGIVNGLYI 60
 OY 64 GYQKLRMTDKYRLHLVSADLLFVITLPFWAVDAVANWFGNLCRAVHYITVNL 123
 DB 61 GYQKLRMTDKYRLHLVSADLLFVITLPFWAVDAVANWFGNLCRAVHYITVNL 118
 OY 124 VLLIAFISLDYLAIVHATNSQPRKLLAEKVVYVGVWIPALLITPDIPIANVSEADR 183
 DB 119 VLLIAFISLDYLAIVHATNSQPRKLLAEKVVYVGVWIPALLITPDIPIANVSEADR 163
 OY 184 YICDRYPNDLWVVFQFQIHMGILPGIYLSCYIIISKLSHSGHQKRAKLT 243
 DB 164 YICDRYPNDLWVVFQFQIHMGILPGIYLSCYIIISKLSHSGHQKRAKLT 223
 OY 244 LIAFACWLPYYIGISIDSIFILEITIKGCEPENTVHKWISTEALAFHCCLANPI 303
 DB 224 LIAFACWLPYYIGISIDSIFILEITIKGCEPENTVHKWISTEALAFHCCLANPI 283
 OY 304 FLGAKFKTSAQHATLSVSRGSSKILSKRGHSSVTESSSFHSS 352
 DB 284 FLGAKFKTSAQHATLSVSRGSSKILSKRGHSSVTESSSFHSS 332

RESULT 4
 09YGC3 PRELIMINARY: PRT: 358 AA.

ID 09YGC3
 AC 09YGC3.
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DE CHEMOKINE RECEPTOR 4.
 GN CXCR4.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Amphibia; Batrachia; Anura;
 OC Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MOERPS B., KNOEPFLE K., BROWN M., KNOEHEL W., GIERSCHIK P.;
 RT "Expression of the CXc chemokine receptor 4 during early Xenopus
 laevis embryogenesis: a possible role of chemokine receptors as
 regulators of development and differentiation."
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: Y17895; CAA76924.1; -.
 DR EMBL: Y17894; CAA76923.1; -.
 DR PROSITE: PS00237; G-PROTEIN_RECEPTOR; 1.
 KW Receptor; G-protein coupled receptor; Transmembrane; Glycoprotein.
 SQ SEQUENCE 358 AA; 40078 MW; E991FD1D CRC32;

Query Match 75.7%; Score 1386; DB 13; Length 358;
 Best Local Similarity 75.1%; Pred. No. 7.1e-104;

	Matches	265	Conservative	36	Mismatches	48	Indels	4	Gaps	2
OY	3	GISITSDNYTEEMSGDYDSKKEPCFREANANKFLPTIYSIIITLGTGVNGNLVILY	62							
			:		:		:		:	
Db	7	GIDINIFDQSNTEENSGDFEDEFIECPFMHNSDDFNRIPLPTIYSFIITLGIITGNGLVVV	66							
OY	63	MOYOKKLRBMTECKYRLHLTSVADLLVITLPEFAVDVAMVWYNGNPLCKRKHVHIYYNLTLS	122							
			:		:		:		:	
Db	67	MOYOKKSRMTMDKYRLHLTSVADLLVETLPEFMSVDAIIGWYKEPELCKRKHVHIYYNLTLS	126							
OY	123	SVLIATFISLIDRYLAIVHAATNSQRPRLKLAEEVYVGVVPIPALLLTIPFIFANVSEAD	182							
			:		:		:		:	
Db	127	SVLIATFISLIDRYLAIVHAATNSQSRKMLADKYVAVGWLPPALLLTLPVLVARRASDENG	186							
OY	183	RYICDRFPY--NDLMVYVVEFOHIMVGLIDPGVILSCYCIISLTSKSHKHOKRKALK	239							
		:::	:		:		:		:	
Db	187	GVCCDRIVPIENREIMVTGVFRFLHTITVGLIDPLGLIILTCYIISLTSKSHKHOKRKALK	246							
OY	240	TTVILILIAFFACWLPYYIGISIDISTLLEFIIOGCEFEVNTVKRWISTETALAFPHCCLP	299							
			:		:		:		:	
Db	247	TTVILILIAFFACWLPYYVCLTIDTFMLLGLVAGDCIMENTLMAISITETALAFPHCCLP	306							
OY	300	ILYAEIAGKFKTSSAOHALTSVRSGSSIKLTSKGRKGHSHSVTESSSSSFHSS	352							
			:		:		:		:	
Db	307	ILYAEIAGKFKTSSAONALFVSRRGSSKLKLS--KRGGLSSVSTESSSSSFHSS	358							

RESULT	5		
042445			
ID	042445	PRELIMINARY:	PRT: 357 AA.
AC	042445:		
DT	01-JAN-1998	(TREMBLrel. 05, Created)	
DT	01-NOV-1998	(TREMBLrel. 08, Last sequence update)	
DT	01-MAY-1999	(TREMBLrel. 10, Last annotation update)	
DE	CXC CHEMOKINE RECEPTOR.		
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;		
OC	Neopterygii; Teleostei; Euteleostei; Protacanthopterygii;		
OC	Salmoniformes; Salmonidae; Oncorhynchus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	DANIELS G.D., CHARLEMAGNE J., SECOMBS C.J.:		
RT	"Cloning and sequencing of a rainbow trout, Oncorhynchus mykiss,		
RT	chemokine receptor homolog.";		
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.		
CC	-1- SUBCELLULAR LOCATION: INTERAL MEMBRANE PROTEIN (BY SIMILARITY)		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
DR	EMBL: AJ001039; CAA04493.1; -		
DR	PFAM: PF00001; 7tm.1.1.		
DR	PROSITE: PS00237; G_PROTEIN_RECEPTOR. 1.		
DR	G-Protein coupled receptor; Transmembrane; Glycoprotein.		
SQ	SEQUENCE 357 AA: 39817 MW: 608925FE CR032:		

Query Match	63.48	Score 1161	DB 13	Length 357
Best Local Similarity	64.58	Pred. No. 8e-86		
Matches 225	Conservative 50	Mismatches 64	Indels 10	Gaps 7

[illegible][illegible]

RESULT	6		
093247			
ID	093247	PRELIMINARY;	PRT; 353 AA.
AC	093247/;		
DT	01-NOV-1998 (TrEMBLrel. 08, Created)		
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)		
DT	01-MAY-1999 (TrEMBLrel. 10, Last annotation update)		
DE	CXCR4.		
OS	Cyprinus carpio (Common carp).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;		
OC	Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;		
OC	Cyprinoidae; Cyprinidae; Cyprininae; Cyprinus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	PUTIKI K., NAKAO M., SHIN D., YANO T.;		
RL	"cDNA cloning of a carp homologue of mammalian CXCR4.";		
RT	Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
DR	EMBL: AB012310; BAA32197.1; -.		
DR	PFAM: PF00001; 7tm.1; 1.		
DR	PROSITE; PS00237; G-PROTEIN-RECEPTOR. 1.		
KW	G-Protein coupled receptor; Transmembrane; Glycoprotein.		
QW	SEQUENCE 353 AA; 39633 MW; 23DD5347 CRC32;		

Query Match	61.3%	Score 1121.5	DB 13	Length 353
Best Local Similarity	64.1%	Pred. No. 1.12e-82		
Matches 223, Conservative	49	Mismatches 67	Indels 9	Gaps 7

[illegible]

RESULT	7	
088410		
ID	088410	PRELIMINARY;
AC	088410;	PRT; 367 AA.
DT	01-NOV-1998	(REMBLrel. 08; Created)
DT	01-NOV-1998	(REMBLrel. 08; Last sequence update)
DT	01-MAY-1999	(REMBLrel. 10; Last annotation update)
DE		CHEMOKINE RECEPTOR CXCR4.


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Db 242 HBAIRVIAVVLVFLACQIPH-----NMVLTAANTKRGVSGCTENVLAATRVAAVY 295
OY 290 LAFFHCCLNPILYAFAGFKTSAOHALTSVSRGSSKLKLS-----KGRGSHSVST 342
Db 296 LAFLHCCLNPILYAFAGFKT-----RNYFMKIMKDVCMRRKMKMGFICANV 343
OY 343 ESES 346
Db 344 YSES 347

RESULT 10
097571 PRELIMINARY: PRT: 356 AA.
AC 097571:
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE INTERLEUKIN-8 RECEPTOR.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Euteria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRED BEAGLE;
RA CHANG Y.F., NOVOSSEL V., CHANG C.F.;
RT "The isolation and sequence of canine interleukin-8 receptor
RL Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF047047; AAC98968.1; -.
KM Receptor.
SQ SEQUENCE 356 AA; 40505 MW; C2B7961F CRC32;

Query Match 30.8%; Score 564; DB 6; Length 356;
Best Local Similarity 35.2%; Pred. No. 6.2e-38;
Matches 128; Conservative 69; Mismatches 129; Indels 38; Gaps 9;

OY 10 DNYTEEMSGDYDSM-----KEPCFREANANKIFLPITYSIITLGTGVNG 57
Db 7 DNYTEEDLEFGDIDNTYNTDMPDIPADSNP-C-RPESLDINKYAAVVIVLVFLNLLGNS 65
OY 58 LVILVMGYOKRLRMTDKYRLHLSVADLFLVITLPEFAVDAVANMYGFNLCRAVHIYT 117
Db 66 LVIMVVLVSRVSHSTDYVLLNLATLADLLFALTLPIWASVKWGFGLPKIYSLE 125
OY 118 VNLVSSVLLAFISLDRIYAIVHATNSQRPRLAEKVYVGVWIPALLITPFIAN- 177
Db 126 VNFYSGILLASISMDRYLAIVHATRLRLOKRWV-KFICLGIWALSLILSPIFVFRRA 184
OY 177 VSEADRYICDRFYNDLWVVFQFOHIM-----VGLLPGVILSCCIIISKLSHG 230
Db 185 IMPPISSPYC-----YEDKNTNTTKLIVKRALPOTFGFVPLMIMFCYGLTLRLTFE 240
OY 231 GHOKRAKLTIVILLAFACWLPYVIGISIDSFILLEIKOGCEPENTVHKWISTEAL 290
Db 241 MQOKRAHRAVIAVAVLVFLCWLPR--NLVADTLMRLOAIEETCCORNDIGALDTELL 298
OY 291 AFFHCCCLNPILYAFAGFKT-----KTSOHALTSVSRGSSKLKLSGKRGSHSVSTESE 345
Db 299 GFHSCCLNPILYAFIGOKFRHGLKIMAFHGLI-----SKREYLPDRSPEFVGSSANT 352
OY 346 SSSF 349
Db 353 STTF 356

RESULT 11
093281 PRELIMINARY: PRT: 392 AA.
ID 093281:
AC 093281:
DT 01-NOV-1998 (TREMBlrel. 08, Created)

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DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE PUTATIVE CHEMOKINE RECEPTOR.
GN CRL.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98244380.
RA GUPTA S.K., PILARISETTI K., GRAY S.L., STADEL J.M.;
RT "Molecular cloning of a novel chemokine receptor-like gene from early
RT stage chick embryos."
RL Biochem. Mol. Biol. Int. 44:673-681(1998).
DR EMBL; AF029369; AAC23950.1; -.
DR PFAM; PF00001; 7tm_1; 2.
SQ SEQUENCE 392 AA; 44760 MW; 429466D8 CRC32;

Query Match 29.7%; Score 544; DB 13; Length 392;
Best Local Similarity 32.9%; Pred. No. 2.8e-36;
Matches 118; Conservative 83; Mismatches 130; Indels 28; Gaps 10;

OY 7 YTSNTEEMSGDYDSMKPCFRENN--AN----FNKIFPTIYSITFLGTGVNGLY 59
Db 43 YEANTPTSL-EGYF-----CFNPSSLMANORDFPKVIFPLAYILMFVIGTVONALV 95
OY 60 ILVMGYOKRLRMTDKYRLHLSVADLFLVITLPEFAVDAVANMYGFNLCRAVHIYT 119
Db 96 LVILRFRKSRPTTENTNLFILTLAMILLTFPPFSVSESLAGWVGTFCLKLSAVHKIN 155
OY 120 LVSSVLLAFISLDRIYAIVHATNSQRPRLAEKVYVGVWIPALLITPFIANV-S 178
Db 156 FYLHEHAAGLHRYDRIYAIYVAIHTRYKARARSHLTCTAIIWLSLLTLPDLMFEWYT 215
OY 179 EADDRYICDRFY-----NDLWVVFQFOHIMVGLIPGIYILSCYCIISKLSHG 232
Db 216 DSNRSIC--YFPEGHIGNNWAT-RTVHSVGFEPMLVMCYMAIVATLQSQRL 272
OY 233 QKRAKLTIVILLAFACWLPYVIGISIDSFILLEIKOGCEPENTVHKWISTEALAF 292
Db 273 QOKRAVRAVIAVAVLVFLCWLPR--NLVADTLMRLOAIEETCCORNDIGALDTEAL 332
OY 299 FHCCCLNPILYAFAGFKTSAOHALTSVSRGSSKLKLSGKRGSHSVSTESSES 347
Db 333 THCCCLNPILYAFAGFKTSAOHALTSVSRGSSKLKLSGKRGSHSVSTESSES 391

RESULT 12
008707 PRELIMINARY: PRT: 378 AA.
ID 008707:
AC 008707:
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DE 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE CHEMOKINE (C-C) RECEPTOR 9 (BETA-CHEMOKINE RECEPTOR D6).
GN CMKBR9
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C3H;
RA NIBBS R.J.B., WYLLIE S.M., PRAGNELL I.B., GRAHAM G.J.;
RL Submitted (MAY-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; Y12879; CAAT3379.1; -.
DR MGD; MGI:1096320; CMKBR9.
DR PFAM; PF00001; 7tm_1; 1.
SQ SEQUENCE 378 AA; 43255 MW; E19F18F5 CRC32;

Query Match 29.3%; Score 535.5; DB 11; Length 378;
Best Local Similarity 30.7%; Pred. No. 1.3e-35;

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Matches 104; Conservative 84; Mismatches 126; Indels 25; Gaps 7;

```

QY 20 DYDSMKE-----PCFREANFNKIFLPTIYSIFLTGIVGNGLVLMGYOKKLRSMYDK 75
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 23 DYDLDMDTILVCRKDEVLSTFGRVFLPVYSLIFVLGAGNLLILVLSHAPRRRTMEL 82
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 76 YRLHLSVADLLFVITLFPMAVDANVMYFGNFKCAVHYITVNLSSVLLAFISLDYR 135
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 YLLNLAVSNLLFVYTMPMAISVAMHWFGSFLCKVISTIXSINPYCGIFPTCMSLDKY 142
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 136 LAIVHATNSORPRKLAKVYVGVNIPALLITPDIFFANVSEK-DRYICDRPYRN-- 193
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 143 LEIHAOPLRPKAOFNRLNLIVMWTSLAIVPEMFOVIOHTLDGVMHCYADFGSHA 202
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 193 DLWVVFQFOHIMVGLIPGIVILSCY-----CIISKLSHSGHOKRKALKTIVLLAF 248
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 203 TIKWKLRFQNLGFLPLAMIFYSRIGCVLRLRPPGOG-----RALMAALVIVF 258
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 FACWLPYVIGISIDSFILLEIKOCCEPENTVHKWISITELAFHCLNPLLYAFILGAK 308
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 259 FLMWFPYVLTFLHSLDLHFV-GNCEISHRLDYTLQVTESLAFSHCCFTPVLYAFCSHR 317
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 309 FKTSAQHALTSVSGSSSLIKSKRGHSSVSTSESS 347
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 318 FRRYIK-----AFLSVMLRMHQADGTPSSNHSESS 347
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 13
097665
ID 097665 PRELIMINARY; PRT; 356 AA.
AC 097665;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE CHEMOKINE RECEPTOR.
GN CCR8.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecoinae;
OC Macaca.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SPLEEN;
RA MARGULIES B.J., HAUER D.A., CLEMENTS J.E.;
RT "Identification and characterization of thirteen rhesus macaque
RT chemokine receptors and chemokine receptor homologues."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF100205; AAC72403.1;
KW Receptor.
SQ SEQUENCE 356 AA; 41210 MW; 30432E9D CRC32;

Query Match 28.9%; Score 528; DB 6; Length 356;
Best Local Similarity 32.4%; Pred. No. 4.8e-35;
Matches 114; Conservative 75; Mismatches 133; Indels 10; Gaps 6;

```

QY 7 YTSNDYTEEMSGDY-DSMKPCFREANFNKIFLPTIYSIFLTGIVGNGLVLMGY 65
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 YTLDPMSMTMTDYYPBLSRSCGDELQKNDKLLAFYCLLVFSLGSLVILVIV 62
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 66 OKLRSMYDKYRLHLSVADLLFVITLFPMAVDANVMYFGNFKCAVHYITVNLSSVL 125
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 CKRLRNITDIYLLNLALSDLLFVSFPQTYQLDQWVFGVMCKVSGFYIGYSME 122
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 126 ILATISLDRIYLAIVHATNSORPKL-LAEKVYVGVNIPALLITPDIFFANVSEADRY 184
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 FITLMSVDRYLAVVAHVAIVKRTIRMGTTLSLWVLTAIMAIPPLVYFQVASEGV 182
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 185 ICDFEYFNDL-WVWVVFQFOHIMVGLIPGIVILSCYCIISKLSHSGHOKRKALKTIV 242
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 183 QCYSFYNOOTLKKMIFTFEEMNIIIGLLPFIIFMPCYIKILHQLKRONHKKTAIRKIVL 242
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 243 ILIAFACWLPYVIGISIDSFILLEIKOCCEPENTVHKWISITELAFHCLNPLTY 302
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db 243 IIVIASLLFWPPNVNVLFTSLSHMHL-DGCSISQOLNATVTELISTHCCVNPVIV 301

QY 303 AFLGAKRTSAQHALTSVSGSSSLIKSKRGHSSV-STSESSSFSS 352

Db 302 AFVGEKER---KHLSEIFKSCSHIFLYIGROMPRESCCKSCCOOHFFRS 350

RESULT 14
009027

ID 009027 PRELIMINARY; PRT; 382 AA.

AC 009027;

DT 01-JUL-1997 (Tremblrel. 04, Created)

DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)

DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)

DE CCR10-RELATED RECEPTOR.

GN CCR10R.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-SPRAGUE-DAWLEY;

RA BONINI J.A., STEINER D.F.;

RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; U92803; AAB61572.1;

PRFAM; PF00001; 7tm_1.1;

SQ SEQUENCE 382 AA; 43293 MW; 74F6D321 CRC32;

Query Match 28.8%; Score 526.5; DB 11; Length 382;
Best Local Similarity 31.1%; Pred. No. 6.8e-35;
Matches 111; Conservative 80; Mismatches 131; Indels 35; Gaps 9;

QY 3 GISITSDNTEEMSGSDYDSMKE-----PCFREANFNKIFLPTIYSIFLTGIVGNGL 58

Db 18 GSSIV-----DYDLDMDTILVCRKDEVLSTFGRVFLPVYSLIFVLGAGNLL 65

QY 59 VILWGVY-KLRSMYDKYRLHLSVADLLFVITLFPMAVDANVMYFGNFKCAVHYIT 117

Db 66 LVVYLHSPQRRKMTIELYLLNLAVSNLLFVYTMPMAISVAMHWFGSLCKVSTLS 125

QY 118 VNLSSVLLAFISLDRIYLAIVHATNSORPKLAEKVYVGVNIPALLITPDIFFANV 177

Db 126 INFQCGIFFTCMSLDKXELIVHAQPLHRKRTFRNLLILVWMTALAVSPEMVFVY 185

QY 178 SEA-DDRYICDRPYRN-DLWVVFQFOHIMVGLIPGIVILSCY-----CIISKLSH 230

Db 186 HQTLDGVMHCYADFGGHATIMKLYLRFQNMNLGFLPLAMIFYSRIGCVLRLRPPG 245

QY 231 GHOKRKALKTIVLLIAFACWLPYVIGISIDSFILLEIKOCCEPENTVHKWISITEL 290

Db 246 G-----RALMAALVYVFFLIMFPYNTLFLHSLDLHFV-GCKKISHRLDYMLQVTEST 300

QY 291 AFHCCINPLIYAFILGAKFKTSAQHALTSVSGSSSLIKSKRGHSSVSTSESS 347

Db 301 AFSHCCFTPVLYAFSSHSFQYLVKAVLSVLR-----RHQAGTAHAPPCSHSESS 351

RESULT 15
055193

ID 055193 PRELIMINARY; PRT; 373 AA.

AC 055193;

DT 01-JUN-1998 (Tremblrel. 06, Created)

DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)

DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)

DE C-C CHEMOKINE RECEPTOR TYPE 2 (C-C CKR-2) (CC-CCR-2) (CCR-2) (CCR2).

GN Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

OC Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

RN [1]

RP SEQUENCE FROM N.A.

RC	STRAIN:SPRAGUE DAWLEY;	
RX	MEDLINE: 98318173.	
RA	JING Y., SALAPANCA M.N., ADHICARI S., XIA Y., FENG L., SONNTAG M.K.,	
RA	DELEIRE C.M., PENNELL N.A., STREIT W.J., HARRISON J.K.;	
RT	"Chemokine receptor expression in cultured gila and rat experimental	
RT	allergic encephalomyelitis."	
RL	J. Neuroimmunol. 86:1-12(1998).	
CC	-I- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5	
CC	CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR	
CC	CALCIUM IONS LEVEL (BY SIMILARITY).	
CC	-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL)	
CC	-I- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SPLEEN, KIDNEY, THYMUS AND	
CC	MACROPHAGES.	
CC	-I- INDUCTION: IN ANIMALS IN WHICH EXPERIMENTAL ALLERGIC	
CC	ENCEPHALOMYELITIS (EME) HAS BEEN INDUCED.	
CC	-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.	
DR	EMBL: U77349; AAC03242.1; .	
DR	PROSITE: PS00237; G.22237; .	
DR	PFAM: Pf00001; 7tm_1.1; 1.	
KW	G-protein coupled receptor; Transmembrane.	
FT	DOMAIN 1 60	
FT	TRANSMEM 61 81	
FT	DOMAIN 82 91	
FT	TRANSMEM 92 112	
FT	DOMAIN 113 128	
FT	TRANSMEM 129 149	
FT	DOMAIN 150 170	
FT	TRANSMEM 171 191	
FT	DOMAIN 192 220	
FT	TRANSMEM 221 241	
FT	DOMAIN 242 256	
FT	TRANSMEM 257 277	
FT	DOMAIN 278 301	
FT	TRANSMEM 302 322	
FT	DOMAIN 323 373	
FT	DISULFID 126 203	
QO	SEQUENCE 373 AA: 42763 MW: 1457808 CRC32:	
	BY SIMILARITY.	

Query Match	28.5%	Score	521.5	DB	11	Length	373
Best Local Similarity	34.9%	Pred	No. 1.7e-34				
Matches	107	Conservative	67	Mismatches	116	Indels	17
						Gaps	8

QY 14 EEMSG-----DYOSMKPCFREENANFNKLFPLTYSIIPLTGIINGVGLIWMGYOK 68

Db 27 QELDEGATTPPYDD-GERCHKYSVKOGAIIPLPISLYIFRFGNMLYIIISCKR 85

QY 69 LRSMTDKRLHLSVADLLFVITLPPMAVDAYANNFCGNLCKAAHVITYNLVSSVTLA 128

Db 86 LKSMIDILFNLAIISDLFLTLTLPFMAHYANENWFGIMCKLTGLTHIDYFEGIEFII 145

QY 129 FISLDRIYAIYHATNSOPRKLAEKVYVGVWVIRALLTLTPDFIPANVSADRYICDR 188

Db 146 LITIDRIYAIYHAFALKARTVITGVIISVTVWVAVFASLPGIITFKSEDDQHTGCR 205

QY 189 FYRPNDLVWVQFOHIM--VGLIPGIVILSCYIIISKLSKSHQKR-KALKTTVIL 244

Db 206 YEPFLIMK--NFOTIMNIIISLPLCLVWVICYSGLIHTFRCKNEKKRRRAVRLIFAI 261

QY 245 ILAFAACFLPYRIGISIDISFILLEI-KOGEFENYVAKWISITEALAFKSCNPILYA 303

Db 262 MIYVFLFMTPRNYVLFLLTF--QELGSLGNSNVDMHLDQANQVETLGMTHSCVNPILYA 319

QY 304 FLGAKFK 310

Db 320 FVGEKFR 326

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 14, 1999, 09:52:22 ; Search time 10.44 Seconds

(without alignments)
953.107 Million cell updates/sec

Title: US-09-104-063-4
Perfect score: 1830
Sequence: 1 MEGISTYTDNTEEMSGSD.....KRGHSSVTESSSSFHSS 352

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database: SwissProt_37.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1830	100.0	352	1 CCR4_HUMAN	P30991 homo sapien
2	1813	99.1	352	1 CCR4_PAPAN	P56491 papio anubi
3	1806	98.7	352	1 CCR4_MACFA	Q28474 macaca fasc
4	1803	98.5	352	1 CCR4_MACMU	P79334 macaca mula
5	1795	98.1	352	1 CCR4_CERTO	O62147 cercocebus
6	1741.5	95.2	353	1 CCR4_FELICA	P56498 felis silve
7	1722.5	94.1	353	1 CCR4_BOVIN	P25930 bos taurus
8	1678.5	91.7	359	1 CCR4_MOUSE	P70658 mus musculu
9	1673	91.4	349	1 CCR4_RAT	O08565 rattus norv
10	934.5	51.1	192	1 CCR4_SHEEP	Q28553 ovis aries
11	600.5	32.8	360	1 CCR4_HUMAN	P51679 homo sapien
12	581.5	31.8	359	1 IL8B_RAT	P35407 rattus norv
13	576.5	31.5	368	1 CCR3_HUMAN	P49682 homo sapien
14	568	31.0	360	1 IL8B_HUMAN	P25025 homo sapien
15	567	31.0	353	1 IL8B_MACMU	Q28519 macaca mula
16	566.5	31.0	353	1 IL8B_GORGO	Q28422 gorilla gor
17	566	30.9	353	1 IL8B_PANTR	Q28807 pan troglod
18	564.5	30.8	350	1 CCR4_MOUSE	P51680 mus musculu
19	564	30.8	360	1 IL8A_RABIT	P21109 oryctolagus
20	563.5	30.8	350	1 IL8A_GORGO	P55919 gorilla gor
21	563.5	30.8	350	1 IL8A_PANTR	P55920 pan troglod
22	563	30.8	378	1 CCR7_MOUSE	P47774 mus musculu
23	558	30.5	358	1 IL8B_RABIT	P35344 oryctolagus
24	557.5	30.5	357	1 GC96_HUMAN	P51686 homo sapien
25	557.5	30.5	350	1 IL8A_HUMAN	P25024 homo sapien
26	557	30.4	378	1 CCR7_HUMAN	P32248 homo sapien
27	549.5	30.0	355	1 GPRD_HUMAN	P49338 homo sapien
28	540	29.5	372	1 BLR1_HUMAN	P32302 homo sapien
29	539	29.5	359	1 IL8B_MOUSE	P35342 mus musculu
30	536	29.3	374	1 BLR1_MOUSE	P35342 mus musculu
31	533.5	29.2	374	1 CCR6_HUMAN	Q04683 homo sapien
32	533.5	29.2	353	1 CCR8_MOUSE	P51684 mus musculu
33	529	28.9	374	1 BLR1_RAT	P34997 rattus norv
34	528	28.9	374	1 CCR2_HUMAN	P41597 homo sapien
35	527	28.8	342	1 BONZ_CERAE	O18883 cercopithec
36	527	28.8	355	1 CCR8_HUMAN	P51685 homo sapien
37	525.5	28.7	342	1 BONZ_MACNE	O19024 macaca neme
38	524.5	28.7	342	1 BONZ_HUMAN	O00574 homo sapien
39	523	28.5	360	1 IL8B_BOVIN	Q28003 bos taurus
40	521.5	28.4	349	1 IL8A_RAT	P70612 rattus norv
41	519.5	28.4	373	1 CCR2_MOUSE	P51683 mus musculu
42	516	28.2	352	1 CCR5_MOUSE	P56493 cercopithec
43	514.5	28.1	354	1 GPRD_RAT	P35411 rattus norv

ALIGNMENTS

44	512	28.0	352	1 CCR5_PANTR	P56440 pan troglod
45	509	27.8	352	1 CCR5_GORGO	P56439 gorilla gor
RESULT 1					
CCR4_HUMAN					
ID	CCR4_HUMAN	STANDARD;	PRT;	352 AA.	
AC	P30991; P56438;				
DT	01-JUL-1993 (REL. 26, CREATED)				
DT	01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)				
DT	15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)				
DE	C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)				
DE	(STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (LCR1) (FB22) (NPR1) (HM89).				
DE	CXCR4.				
GN	CXCR4.				
OS	HOMO SAPIENS (HUMAN), AND PAN TROGLODYTES (CHIMPANZEE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;				
OC	PRIMATES; CATARRHINI; HOMINIDAE; HOMO.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES-HUMAN: TISSUE=LUNG;				
RX	MEDLINE: 93319629.				
RA	HERZOG H., HORT Y.J., SHINE J., SELBIE L.A.;				
RT	"Molecular cloning, characterization, and localization of the human homolog to the reported bovine NPY Y3 receptor: lack of NPY binding and activation."				
RT	DNA CELL BIOL. 12:465-471(1993).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES-HUMAN: TISSUE=BRAIN;				
RX	MEDLINE: 94052833.				
RA	JAZIN E.E., YOO H., BLOMOVIST G., YEE F., WENG G., WALKER M.W.,				
RA	SALON J., LARHAMMAR D., WAHLESTEDT C.R.;				
RT	"A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human homologue, confers neither NPY binding sites nor NPY responsiveness on transfected cells."				
RT	REGUL. PEPT. 47:247-258(1993).				
RL	GENOTCS 16:707-712(1993).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES-HUMAN: TISSUE=SPLEEN;				
RX	MEDLINE: 93315164.				
RA	FEDERSPIEL B., DELANEY A.D., CLARK-LEWIS I., JIRIK F., DUNCAN A.M.,				
RA	SCHAPPERT K.T., MELIADO I.;				
RT	"Molecular cloning of the cDNA and chromosomal localization of the RT gene for a putative seven-transmembrane segment (7-TMS) receptor isolated from human spleen."				
RT	GENOTCS 16:707-712(1993).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES-HUMAN: TISSUE=LEUKOCYTE;				
RX	MEDLINE: 94103215.				
RA	LOEWSCHER M., GEISER T., O'REILLY T., ZWAHLN R., BAGGIOLINI M.,				
RA	MOSER B.;				
RT	"Cloning of a human seven-transmembrane domain receptor, LESTR, that is highly expressed in leukocytes."				
RT	J. BIOL. CHEM. 269:232-237(1994).				
RL	[5]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES-HUMAN: TISSUE=MONOCYTES;				
RX	MEDLINE: 94092629.				
RA	NOMURA H., NIELSEN B.W., MATSUSHIMA K.;				
RT	"Molecular cloning of cDNAs encoding a ID78 receptor and putative leukocyte chemotactic peptide receptors."				
RT	INT. IMMUNOL. 5:1239-1249(1993).				
RN	[6]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES-HUMAN;				
RA	WEGNER S.A., EHRENBERG P.K., CHANG G., DAYHOFF D.E., MICHAEL N.L.;				
RT	SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.				

[7]
 RN SEQUENCE FROM N.A.
 RP SPECIES-P.TROGLODYTES;
 RX MEDLINE: 98090115.
 RA PRETET J.-L., ZEBIB A., GIRARD M., GUILLET J.-G., BUTOR C.;
 RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
 RL AIDS RES. HUM. RETROVIRUSES 13:1583-1587(1997).
 [8]
 RN FUNCTION.
 RP MEDLINE: 96351077.
 RA BLEUL C.C., FARZAN M., CHOE H., PAROLIN C., CLARK-LEWIS I.,
 RT SODROSKI J., SPRINGER T.A.;
 RL "The lymphocyte chemottractant SDF-1 is a ligand for LESTR/fusin and
 blocks HIV-1 entry.";
 RL NATURE 382:829-833(1996).
 [9]
 RN FUNCTION.
 RP MEDLINE: 96351078.
 RA OBERLIN E., AMARA A., BACHELERIE F., BESSIA C., VIRELIZIER J.-L.,
 RA ARENZANA-SEISDEDES F., SCHWARTZ O., HEARD J.-M., CLARK-LEWIS I.,
 RA LEGIER D.F., LOETSCHER M., BAGGIOLINI M., MOSER B.;
 RT "The CXCR4 chemokine SDF-1 is the ligand for LESTR/fusin and prevents
 infection by T-cell-line-adapted HIV-1.";
 RL NATURE 382:833-835(1996).
 [10]
 RN ERRATUM.
 RA OBERLIN E., AMARA A., BACHELERIE F., BESSIA C., VIRELIZIER J.-L.,
 RA ARENZANA-SEISDEDES F., SCHWARTZ O., HEARD J.-M., CLARK-LEWIS I.,
 RA LEGIER D.F., LOETSCHER M., BAGGIOLINI M., MOSER B.;
 RL NATURE 384:288-288(1996).
 [11]
 RN CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RA MEDLINE: 9621947.
 RA FENG Y., BRODER C.C., KENNEDY P.E., BERGER E.A.;
 RT "HIV-1 entry cofactor: functional cDNA cloning of a
 seven-transmembrane, G protein-coupled receptor.";
 RL SCIENCE 272:872-877(1996).
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- FUNCTION: ACTS AS AS CO-RECEPTOR WITH CD4 FOR SYNCTIUM-INDUCING
 STRAINS (SI) (T-CELL-LINE-ADAPTED) OF HIV-1 VIRUS. IT PROMOTES
 ENV-MEDIATED FUSION OF THE VIRUS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -1- CUTION: WAS ORIGINALLY THOUGHT TO BE A RECEPTOR FOR NEUROPEPTIDE
 Y. TYPE 3 (NPY3-R).
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: L01639; G189314; -
 DR EMBL: M99293; G292517; -
 DR EMBL: X71635; G297100; -
 DR EMBL: L06797; G414928; -
 DR EMBL: D10924; -; NOT_ANNOTATED_CDS.
 DR EMBL: AF005058; G2735719; -
 DR EMBL: U89798; G2281447; -
 DR PIR: S32761; S32761.
 DR PIR: A45747; A45747.
 DR GCRDB: GCR_0438; -
 DR GCRDB: GCR_0448; -
 DR GCRDB: GCR_0475; -
 DR GCRDB: GCR_0529; -
 DR GCRDB: GCR_0903; -
 DR GCRDB: GCR_2433; -
 DR GCRDB: GCR_2568; -
 DR MIM: 162643; -
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.

DR PFAM: PF00001; 7tm.1; 1.
 KM G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE: GLYCOPROTEIN.
 FT DOMAIN 1 39
 FT TRANSMEM 40 63
 FT DOMAIN 64 79
 FT TRANSMEM 80 99
 FT DOMAIN 100 110
 FT TRANSMEM 111 132
 FT DOMAIN 133 154
 FT TRANSMEM 155 175
 FT DOMAIN 176 200
 FT TRANSMEM 201 220
 FT DOMAIN 221 240
 FT TRANSMEM 241 261
 FT DOMAIN 262 285
 FT TRANSMEM 286 305
 FT DOMAIN 306 352
 FT CARBOHYD 11 11
 FT DISULFID 109 186
 SQ SEQUENCE 352 AA; 39745 MW; BDE02133 CRC32;
 Query Match 100.0%; Score 1830; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1,8e-117;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEGISTYSDNTEEMSGSDYDSMKPECFRENNANENKIFLPTYSIFLGLVNGGLVI 60
 DB 1 MEGISTYSDNTEEMSGSDYDSMKPECFRENNANENKIFLPTYSIFLGLVNGGLVI 60
 QY 61 LVNGYOKLRSMTDKYRLHLSVADLLFVTTPMAVDAANMYFGNGLCAVAVITYVL 120
 DB 61 LVNGYOKLRSMTDKYRLHLSVADLLFVTTPMAVDAANMYFGNGLCAVAVITYVL 120
 QY 121 YSSVLIAFLISDRYLAIYHATNSQPRKLAKEVYVGVWIPALLITPDEFANVSEA 180
 DB 121 YSSVLIAFLISDRYLAIYHATNSQPRKLAKEVYVGVWIPALLITPDEFANVSEA 180
 QY 121 YSSVLIAFLISDRYLAIYHATNSQPRKLAKEVYVGVWIPALLITPDEFANVSEA 180
 DB 121 YSSVLIAFLISDRYLAIYHATNSQPRKLAKEVYVGVWIPALLITPDEFANVSEA 180
 QY 181 DRYICDRFPNDLWVYVFOFHIMGLIPGIVILSCYCIILSKLSHGQKRRAKT 240
 DB 181 DRYICDRFPNDLWVYVFOFHIMGLIPGIVILSCYCIILSKLSHGQKRRAKT 240
 QY 241 TVLLILAFACMLPYIIGISIDFILLITIKOGCEFNHVMISTELAFHCCLNPI 300
 DB 241 TVLLILAFACMLPYIIGISIDFILLITIKOGCEFNHVMISTELAFHCCLNPI 300
 QY 301 LVAFIAKFKTSQNALTSVSRGSSSLKILSKGRGSHSVSTESSSPHSS 352
 DB 301 LVAFIAKFKTSQNALTSVSRGSSSLKILSKGRGSHSVSTESSSPHSS 352
 RESULT 2
 CCR4_PAPAN STANDARD; PRI: 352 AA.
 AC P56491;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN).
 GN CXCR4.
 OS PAPIO ANUBIS (OLIVE BABOON).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; CERCOPITHECIDAE; CERCOPITHECINAE; PAPIO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BENTON P.A., TIMANUS D.K., SHEARER M.H., LEE D.R., KENNEDY R.C.;
 RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----

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 CC or send an email to license@isb-sib.ch).

DR EMBL: AF031089; G2625094; -
 DR GCRDB: GCR_2512; -
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
 FT DOMAIN 1 39
 FT TRANSMEM 40 63
 FT DOMAIN 64 79
 FT TRANSMEM 80 99
 FT DOMAIN 100 110
 FT TRANSMEM 111 132
 FT DOMAIN 133 154
 FT TRANSMEM 155 175
 FT DOMAIN 176 200
 FT TRANSMEM 201 220
 FT DOMAIN 221 240
 FT TRANSMEM 241 261
 FT DOMAIN 262 285
 FT TRANSMEM 286 305
 FT DOMAIN 306 352
 FT CARBOHYD 11 11
 FT DISULFID 109 186
 SQ SEQUENCE 352 AA; 39751 MW; 273DB8BE CRC32;

Query Match 99.1%; Score 1813; DB 1; Length 352;
 Best Local Similarity 98.9%; Pred. No. 2.6e-116;
 Matches 348; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGISITYSDNTTEEMSGDYDMSKEPCFEENANFNKIFPTIYSIFLTGIVGNGLY 60
 DB 1 MEGISITYSDNTTEEMSGDYDMSKEPCFEENANFNKIFPTIYSIFLTGIVGNGLY 60
 QY 61 LVNGYOKKLRSMTDKRYRLHLSVADLLFVITLPPWAVDAVANMFGNFKCAVHYITVNL 120
 DB 61 LVNGYOKKLRSMTDKRYRLHLSVADLLFVITLPPWAVDAVANMFGNFKCAVHYITVNL 120
 QY 121 YSSVLLAFISIDRYLAIVHATNSORPKRLAEKVYVGVWIPALLTTPDFFAVNSEA 180
 DB 121 YSSVLLAFISIDRYLAIVHATNSORPKRLAEKVYVGVWIPALLTTPDFFAVNSEA 180
 QY 181 DORYICDREFYNDLWVVFQFOHIMVGLIPGIVILSCYCIISKLSSHSGHQRKRLAKT 240
 DB 181 DORYICDREFYNDLWVVFQFOHIMVGLIPGIVILSCYCIISKLSSHSGHQRKRLAKT 240
 QY 241 TYVLLIAFACWLPYYIGISIDSFILLEITIKOCCEFEENVHKWISTEALAFHCLNPI 300
 DB 241 TYVLLIAFACWLPYYIGISIDSFILLEITIKOCCEFEENVHKWISTEALAFHCLNPI 300
 QY 301 LYAFILAKFKTSQAHALTSVSRGSSSLIKSKRGKRGHSSVTESSSSPHSS 352
 DB 301 LYAFILAKFKTSQAHALTSVSRGSSSLIKSKRGKRGHSSVTESSSSPHSS 352

RESULT 3
 CCR4_MACFA STANDARD; PRT: 352 AA.
 ID CCR4_MACFA
 AC 028474;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 GN (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (LESTR).
 OS MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLUS MONKEY).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:

OC PRIMATES; CATARRHINI; CERCOPITHECIDAE; CERCOPITHECINAE; MACACA.
 RN [1]
 RA SEQUENCE FROM N.A.
 RP TATSUMI M., TAKAHASHI H.;
 RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL: D86579; G1468949; -
 DR GCRDB: GCR_1143; -
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.
 KW PFAM: PF00001; 7tm_1; 1.
 FT G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
 FT DOMAIN 1 39
 FT TRANSMEM 40 63
 FT DOMAIN 64 79
 FT TRANSMEM 80 99
 FT DOMAIN 100 110
 FT TRANSMEM 111 132
 FT DOMAIN 133 154
 FT TRANSMEM 155 175
 FT TRANSMEM 176 200
 FT DOMAIN 201 220
 FT TRANSMEM 221 240
 FT DOMAIN 241 261
 FT TRANSMEM 262 285
 FT DOMAIN 286 305
 FT CARBOHYD 11 11
 FT DISULFID 109 186
 SQ SEQUENCE 352 AA; 39753 MW; 7EDA93BA CRC32;

Query Match 98.7%; Score 1805; DB 1; Length 352;
 Best Local Similarity 98.3%; Pred. No. 7.6e-116;
 Matches 346; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEGISITYSDNTTEEMSGDYDMSKEPCFEENANFNKIFPTIYSIFLTGIVGNGLY 60
 DB 1 MEGISITYSDNTTEEMSGDYDMSKEPCFEENANFNKIFPTIYSIFLTGIVGNGLY 60
 QY 61 LVNGYOKKLRSMTDKRYRLHLSVADLLFVITLPPWAVDAVANMFGNFKCAVHYITVNL 120
 DB 61 LVNGYOKKLRSMTDKRYRLHLSVADLLFVITLPPWAVDAVANMFGNFKCAVHYITVNL 120
 QY 121 YSSVLLAFISIDRYLAIVHATNSORPKRLAEKVYVGVWIPALLTTPDFFAVNSEA 180
 DB 121 YSSVLLAFISIDRYLAIVHATNSORPKRLAEKVYVGVWIPALLTTPDFFAVNSEA 180
 QY 181 DORYICDREFYNDLWVVFQFOHIMVGLIPGIVILSCYCIISKLSSHSGHQRKRLAKT 240
 DB 181 DORYICDREFYNDLWVVFQFOHIMVGLIPGIVILSCYCIISKLSSHSGHQRKRLAKT 240
 QY 241 TYVLLIAFACWLPYYIGISIDSFILLEITIKOCCEFEENVHKWISTEALAFHCLNPI 300
 DB 241 TYVLLIAFACWLPYYIGISIDSFILLEITIKOCCEFEENVHKWISTEALAFHCLNPI 300
 QY 301 LYAFILAKFKTSQAHALTSVSRGSSSLIKSKRGKRGHSSVTESSSSPHSS 352
 DB 301 LYAFILAKFKTSQAHALTSVSRGSSSLIKSKRGKRGHSSVTESSSSPHSS 352

RESULT 4

CCR4_MACMU STANDARD; PRT: 352 AA.

AC P79394; 002745; 046428;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LESTR).
 GN CXCR4.
 OS MACACA MULATTA (RHEBUS MACAQUE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; CERCOPITHECIDAE; CERCOPITHECINAE; MACACA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-INDIAN MACAQUE;
 RX MEDLINE: 97213934.
 RA CHEN Z., ZHOU P., HO D.D., LANDAU N.R., MARX P.A.;
 RT "Genetically divergent strains of simian immunodeficiency virus use CCR5 as a coreceptor for entry.";
 RL J. VIROL. 71:2705-2714(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97268687.
 RA EDINGER A.L., AMEDEE A., MILLER K., DORANZ B.J., ENDRES M.,
 RA SHARRON M., SAMSON M., LU Z.-H., CLEMENTS J.E., MURPHEY-CORB M.,
 RA PIPPER S.C., PARMENTIER M., BRODER C.C., DOMS R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 94:4005-4010(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CHINESE;
 RX MEDLINE: 98252393.
 RA PRETET J.-L., GUILLET J.-G., BUTOR C.;
 RT "New widespread CXCR4 allele in rhesus macaques does not predict subspecies or clinical evolution.";
 RL AIDS RES. HUM. RETROVIRUSES 14:639-641(1998).
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL: U73740; G1899056; -
 CC EMBL: U93311; G1934671; -
 CC EMBL: AF001928; G2911294; -
 DR GCRDB: GCR.1297; -
 DR GCRDB: GCR.1640; -
 DR PROSITE: PS00237; G.PROTEIN_RECEPTOR; 1.
 DR PRAM: PF00001; 7tm.1; 1.
 KM G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
 FT DOMAIN 1 39
 FT TRANSMEM 40 63
 FT DOMAIN 64 79
 FT TRANSMEM 80 99
 FT DOMAIN 100 110
 FT TRANSMEM 111 132
 FT DOMAIN 133 154
 FT TRANSMEM 155 175
 FT DOMAIN 176 200
 FT TRANSMEM 201 220
 FT DOMAIN 221 240
 FT TRANSMEM 241 261
 FT DOMAIN 262 285
 FT TRANSMEM 286 305
 FT DOMAIN 306 352
 CYTOPLASMIC (POTENTIAL).
 7 (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 11 11 POTENTIAL.
 FT DISULFID 109 186 BY SIMILARITY.
 FT CONFLICT 67 67 K -> E (IN REF. 2).
 FT CONFLICT 214 214 D -> V (IN REF. 2 AND 3).
 FT CONFLICT 348 348 S -> N (IN REF. 2).
 SQ SEQUENCE 352 AA; 39739 MW; 3C3344BB CRC32;

Query Match 98.5%; Score 1803; DB 1; Length 352;
 Best Local Similarity 98.3%; Pred. No. 1,2e-115;
 Matches 346; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEGSIYTSNTEEMSGSDYDSMKRCPREANANKIFLPITYSIIFLTGIVNGLYI 60
 DB 1 MEGSIYTSNTEEMSGSDYDSMKRCPREANANKIFLPITYSIIFLTGIVNGLYI 60
 QY 61 LVNGYOKRLSMYDKYRLHLSVADLLFVITLPEMAVDAAVMYFGNLCRAVHYITVL 120
 DB 61 LVNGYOKRLSMYDKYRLHLSVADLLFVITLPEMAVDAAVMYFGNLCRAVHYITVL 120
 QY 121 YSSVLIATFISDRYATYHATNSQRPKRLAEKVYVGVWIPALLITPDLFANVSA 180
 DB 121 YSSVLIATFISDRYATYHATNSQRPKRLAEKVYVGVWIPALLITPDLFANVSA 180
 QY 181 DDRYICDRFPNDLWVYVFOFHIMVGLIPGIVLISCIYISKLSHSGHOKRAKLT 240
 DB 181 DDRYICDRFPNDLWVYVFOFHIMVGLIPGIVLISCIYISKLSHSGHOKRAKLT 240
 QY 241 TVILILAFACWLPYYIGISIDSFILLEITIKOCCEPENTVHKWISTEALAFHCLNPI 300
 DB 241 TVILILAFACWLPYYIGISIDSFILLEITIKOCCEPENTVHKWISTEALAFHCLNPI 300
 QY 301 LVAFLEAKFTSQHALTVSRSSSLIKSKRGHSSVSTSESSSFHSS 352
 DB 301 LVAFLEAKFTSQHALTVSRSSSLIKSKRGHSSVSTSESSSFHSS 352

RESULT 5
 CCR4_CERTO STANDARD; PRT: 352 AA.

ID CCR4_CERTO
 AC 062747;
 DT 15-DEC-1998 (REL. 37, CREATED)
 DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LESTR).
 GN CXCR4.
 OS CERCOCERUS TORQUATUS ATYS (RED-CROWNED MANGABEY) (SOOTY MANGABEY).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; CERCOPITHECIDAE; CERCOPITHECINAE; CERCOCERUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 98321155.
 RA CHEN Z., GETTIE A., HO D.D., MARX P.A.;
 RT "Primary siyem isolates use the CCR5 coreceptor from sooty mangabeys naturally infected in west Africa: a comparison of coreceptor usage of primary siyem, HIV-2 and siyemac.";
 RL VIROLOGY 246:113-124(1998).
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL: AF051906; G3135304; -
 DR PROSITE: PS00237; G.PROTEIN_RECEPTOR; 1.

KM G-PROTEIN COUPLED RECEPTOR: TRANSMEMBRANE: GLYCOPROTEIN.
 FT DOMAIN 1 39
 FT TRANSMEM 40 63
 FT DOMAIN 64 79
 FT TRANSMEM 80 99
 FT DOMAIN 100 110
 FT TRANSMEM 111 132
 FT DOMAIN 113 154
 FT TRANSMEM 155 175
 FT DOMAIN 176 200
 FT TRANSMEM 201 220
 FT DOMAIN 221 240
 FT TRANSMEM 241 261
 FT DOMAIN 262 285
 FT TRANSMEM 286 305
 FT DOMAIN 306 352
 FT CAROHD 11
 FT DISULFID 109
 SQ SEQUENCE 352 AA: 39648 MW: 88464DAD CRC32;

Query Match 98.1%; Score 1795; DB 1; Length 352;
 Best Local Similarity 97.7%; Pred. No. 4.2e-115;
 Matches 344; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

OY 1 MEGISITVSDNTEEMSGSDYDSMKPCFREANANKIFLPTIYSITFLTGIVGNGLY 60
 DB 1 MEGISITVSDNTEEMSGSDYDSMKPCFREANANKIFLPTIYSITFLTGIVGNGLY 60
 OY 61 LVMGYQKRLSRMTDKYRLHLSVADLLFVITLPEFAVDAVANNYFGNFKCAVHIVTVNL 120
 DB 61 LVMGYQKRLSRMTDKYRLHLSVADLLFVITLPEFAVDAVANNYFGNFKCAVHIVTVNL 120
 OY 121 YSSVLLIAFISLDRIALIVHATNSQRPRLAEKYYVGVWIPALLITPDITFANVSA 180
 DB 121 YSSVLLIAFISLDRIALIVHATNSQRPRLAEKYYVGVWIPALLITPDITFANVSA 180
 OY 181 DDRYICDRFPNDLVVWVFOFOHIMVGLILPGIVILSCYCIILSKSHSGHOKRKALKT 240
 DB 181 DDRYICDRFPNDLVVWVFOFOHIMVGLILPGIVILSCYCIILSKSHSGHOKRKALKT 240
 OY 241 TVILILAFACWLPYYIGISIDSIFLLEIKOGCEFEFNVHAKWISTEALAFHCCLANP 300
 DB 241 TVILILAFACWLPYYIGISIDSIFLLEIKOGCEFEFNVHAKWISTEALAFHCCLANP 300
 OY 301 LYAFILGAKFKTSAOHALTSVSRGSSILKILSKGRGHSVSTESSESSPHSS 352
 DB 301 LYAFILGAKFKTSAOHALTSVSRGSSILKILSKGRGHSVSTESSESSPHSS 352

RESULT 6
 CCR4_FELICA STANDARD: PRT: 353 AA.
 AC P36498: P79172: 002700:
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDP-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LESTR).
 GN CXCR4.
 OS FELIS SILVESTRIS CATUS (CAT).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 OC CARNIVORA: FISSIPEDIA: FELIDAE: FELIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97404646.
 RA WILLETT B.J., PICARD L., HOSIE M.J., TURNER J.D., ADEKA K.,
 RA CLAPHAM P.R.;
 RT "Shared usage of the chemokine receptor CXCR4 by the feline and human
 RT immunodeficiency viruses.";
 RL J. VIROL. 71:6407-6415(1997).
 RN [2]
 RP SEQUENCE FROM N.A.

RA WILLETT B.J.;
 RL SUBMITTED (DEC-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA LERNER D.L., ELDER J.H.;
 RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL: U63558; G1842247; -;
 DR EMBL: U92795; G1935045; -;
 DR GCRDB; GCR_1114; -;
 DR GCRDB; GCR_1114; -;
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR: 1.
 KM G-PROTEIN COUPLED RECEPTOR: TRANSMEMBRANE: GLYCOPROTEIN.
 FT DOMAIN 1 40
 FT TRANSMEM 41 64
 FT DOMAIN 65 80
 FT TRANSMEM 81 100
 FT DOMAIN 101 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 155
 FT TRANSMEM 156 176
 FT DOMAIN 177 201
 FT TRANSMEM 202 221
 FT DOMAIN 222 241
 FT TRANSMEM 242 262
 FT DOMAIN 263 286
 FT TRANSMEM 287 306
 FT DOMAIN 307 353
 FT CAROHD 11
 FT DISULFID 110
 FT CONFLICT 67
 FT CONFLICT 263
 SQ SEQUENCE 353 AA: 39935 MW: 5829DIE CRC32;

Query Match 95.2%; Score 1741.5; DB 1; Length 353;
 Best Local Similarity 94.6%; Pred. No. 1.8e-111;
 Matches 334; Conservative 11; Mismatches 7; Indels 1; Gaps 1;

OY 1 MEGISITVSDNTE-EMSGSDYDSMKPCFREANANKIFLPTIYSITFLTGIVGNGLY 59
 DB 1 MEGISITVSDNTE-EMSGSDYDSMKPCFREANANKIFLPTIYSITFLTGIVGNGLY 60
 OY 60 ILVVGQKRLSRMTDKYRLHLSVADLLFVITLPEFAVDAVANNYFGNFKCAVHIVTVN 119
 DB 60 ILVVGQKRLSRMTDKYRLHLSVADLLFVITLPEFAVDAVANNYFGNFKCAVHIVTVN 120
 OY 120 LYSSVLLIAFISLDRIALIVHATNSQRPRLAEKYYVGVWIPALLITPDITFANVSE 179
 DB 120 LYSSVLLIAFISLDRIALIVHATNSQRPRLAEKYYVGVWIPALLITPDITFANVSE 180
 OY 180 ADDRITCDRFYNDLVVWVFOFOHIMVGLILPGIVILSCYCIILSKSHSGHOKRKALK 239
 DB 180 ADDRITCDRFYNDLVVWVFOFOHIMVGLILPGIVILSCYCIILSKSHSGHOKRKALK 240
 OY 240 TVILILAFACWLPYYIGISIDSIFLLEIKOGCEFEFNVHAKWISTEALAFHCCLANP 299
 DB 240 TVILILAFACWLPYYIGISIDSIFLLEIKOGCEFEFNVHAKWISTEALAFHCCLANP 300
 OY 300 ILVAFILGAKFKTSAOHALTSVSRGSSILKILSKGRGHSVSTESSESSPHSS 352

DB 301 ILYAFGAKFKTSAGHALTSVSRGSSSLKILSKGRGSHSVSTESSFSHSS 353

RESULT 7

CCRA_BOVIN 7 STANDARD: PRT: 353 AA.

AC P25930;

DT 01-MAY-1992 (REL. 22, CREATED)

DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)

DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (CXCR-4) (SDF-1 RECEPTOR)

DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (LCR1).

OS CXCR4.

OS BOS TAURUS (BOVINE).

OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:

OC ARTIODACTYLA: RUMINANTIA: PECORA: BOVIDAE: BOVINAE: BOS.

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE-LOCUS COERULEUS;

RL MEDLINE: 92100053.

RA RIMLAND J., XIN W., SWEETNAM P., SALJOH K., NESTLER E.J., DUMAN R.S.;

RT "Sequence and expression of a neuropeptide Y receptor cDNA.";

RL MOL. PHARMACOL. 40:869-875(1991).

RN (2)

RP SHOWS THAT IT IS NOT A NPY3-R.

RL MEDLINE: 94052833.

RA JAZIN E.E., YOO H., BLOMOVIST G., YEE F., WENG G., WALKER M.W.,

RA SALON J., LARHAMMAR D., WAHLESTEDT C.R.;

RT "A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human homologue, confers neither NPY binding sites nor NPY responsiveness on transfected cells.";

RL REGUL. PEPT. 47:247-258(1993).

CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: BRAIN, HEART, KIDNEY, LONG AND LIVER.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -1- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE A RECEPTOR FOR NEUROPEPTIDE Y, TYPE 3 (NPY3-R).

CC -----

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CC -----

CC EMBL: M86739; -; NOT_ANNOTATED_CDS.

DR PIR: S28787; S28787.

DR GCRDB: GCR_0180; -;

DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.

DR PFAM: PF00001; 7tm_1.1.

KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.

KW DOMAIN 1 40

FT TRANSMEM 41 60

FT DOMAIN 65 84

FT TRANSMEM 81 100

FT DOMAIN 101 111

FT TRANSMEM 112 133

FT DOMAIN 134 155

FT TRANSMEM 156 176

FT DOMAIN 177 201

FT TRANSMEM 202 221

FT DOMAIN 222 241

FT TRANSMEM 242 262

FT DOMAIN 263 286

FT TRANSMEM 287 306

FT DOMAIN 307 353

FT CARBOHYD 11 11

FT DISULFID 110 187

SQ 353 AA; 39938 MW; 03DBF100 CRC32;

Query Match 94.1%; Score 1722.5; DB 1; Length 353;

Best Local Similarity 92.4%; Pred. No. 3.4e-110;

Matches 326; Conservative 20; Mismatches 6; Indels 1; Gaps 1;

QY 1 MEGISYTSNDNTE-EMSGGDYDSMKPECFREBNAFNKIFLPTIYSIFLGIYNGV 59

DB 1 MEDIRLFISDNTIEDDGSDDDSKMEPCFRENHAFNFIPLTYSIIFLGIYNGV 60

QY 60 IIVMGYQKLRSMTDKRYRLSLVADLLFVITLPEMAVDANVMYEGNLCRAVHYTVN 119

DB 61 IIVMGYQKLRSMTDKRYRLSLVADLLFVITLPEMAVDANVMYEGNLCRAVHYTVN 120

QY 120 LYSSVILLAFISLDRLALVHATNSGRPKLLAEKVYVGVWIPALLTIPIPIANSE 179

DB 121 LYSSVILLAFISLDRLALVHATNSGRPKLLAEKVYVGVWIPALLTIPIPIADIE 180

QY 180 ADDRICYDRFPNDLWVVFVFOHIMVGLIPGIVILSCYCIITISKLSHGOKRAK 239

DB 181 VDERYICDRFPYSDMLWVVFVFOHIVGILLPGIVILSCYCIITISKLSHGOKRAK 240

QY 240 TVVILLAFECMLPYIIGISIDSFILIEIRKQGEFFENTVHKWISITELAFHCCLP 299

DB 241 TVVILLAFECMLPYIIGISIDSFILIEIRKQGEFFENTVHKWISITELAFHCCLP 300

QY 300 ILYAFGAKFKTSAGHALTSVSRGSSSLKILSKGRGSHSVSTESSFSHSS 352

DB 301 ILYAFGAKFKTSAGHALTSVSRGSSSLKILSKGRGSHSVSTESSFSHSS 353

RESULT 8

CCRA_MOUSE 7 STANDARD: PRT: 359 AA.

AC P70658; P70346; 009062; 009059; P70233;

DT 01-NOV-1997 (REL. 35, CREATED)

DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (CXCR-4) (SDF-1 RECEPTOR)

DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR).

OS CXCR4 OR LESTR OR CXCR4 OR SDF1R.

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:

OC RODENTIA: SCIUROGNATHI; MURIDAE; MURINAE; MUS.

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN-C57BL/6 X CBA; TISSUE-THYMUS;

RA MOEPPS B., FRODL R., KESSLER H., GIERSCHEK P.;

RL SUBMITTED (NOV-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

RN (2)

RP SEQUENCE FROM N.A.

RC STRAIN-129/SV;

RA HEESSEN M., BERMAN M.A., GERARD C., DORF M.E.;

RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

RN (3)

RP SEQUENCE FROM N.A.

RC STRAIN-C57BL/6J;

RA MEDLINE: 9711334.

RA HEESSEN M., BERMAN M.A., BENSON J.D., GERARD C., DORF M.E.;

RT "Cloning of the mouse fusin gene, homologue to a human HIV-1 co-factor.";

RL J. IMMUNOL. 157:5455-5460(1996).

RN (4)

RP SEQUENCE FROM N.A.

RC TISSUE-BONE MARROW;

RA MEDLINE: 97121456.

RA NAGASAWA T., NAKAJIMA T., TACHIBANA K., IIZASA H., BLEUL C.C.,

RA YOSHIE O., MATSUSHIMA K., YOSHIDA N., SPRINGER T.A., KISHIMOTO T.;

RT "Molecular cloning and characterization of a murine pre-B-cell growth-stimulating factor/stromal cell-derived factor 1 receptor, a murine homolog of the human immunodeficiency virus 1 entry coreceptor fusin.";

```

RL PROC. NATL. ACAD. SCI. U.S.A. 93:14726-14729(1996).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=THYMUS;
RA SUZUKI G., NAKATA Y., UZAWA A., SHIRASAWA T., SAITO T., MITA K.;
RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV; TISSUE=THYMUS;
RA SCHUBEL A., BURGSTALLER R., LIPP M.;
RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; X99581; E281127; -
DR EMBL; X99582; E281126; -
DR EMBL; U59760; G1527135; -
DR EMBL; U65580; G1731651; -
DR EMBL; D87747; G1772446; -
DR EMBL; AB000803; G1816446; -
DR EMBL; 280111; E266602; -
DR GCRDB; GCR_1138; -
DR GCRDB; GCR_1187; -
DR GCRDB; GCR_1646; -
DR GCRDB; GCR_1730; -
DR GCRDB; GCR_2592; -
DR MGI; 109563; CMKAR4.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7tm_1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
FT DOMAIN 1 41
FT TRANSMEM 42 65
FT DOMAIN 66 81
FT TRANSMEM 82 101
FT DOMAIN 102 112
FT TRANSMEM 113 134
FT DOMAIN 135 156
FT TRANSMEM 157 177
FT DOMAIN 178 207
FT TRANSMEM 208 227
FT DOMAIN 228 247
FT TRANSMEM 248 268
FT DOMAIN 269 292
FT TRANSMEM 293 312
FT DOMAIN 313 359
FT DISULFID 111 193
FT CARBOHYD 13 13
FT CONFLICT 6 7
FT CONFLICT 216 216
FT SEQUENCE 359 AA; 40426 MW; 1037BAD3 CRC32;

```

Query Match 91.7%; Score 1678.5; DB 1; Length 359;
 Best Local Similarity 90.1%; Pred. No. 3.3e-107;
 Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

```

OY 4 ISIVTSDNTTEEMSGDYDSMKEPCFREANFNKIFPTIYSIIFLTGIVNGIIVLM 63
DB 6 VSIYSDNYSSEVSGDYDSMKEPCFREANFNKIFPTIYSIIFLTGIVNGIIVLM 65
OY 64 GYOKKLRSMTDKRYRLHLSTADLLFVITLPEFAVDAMNMFNGFLCKAVHVIYTNLYSS 123

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DB 66 GYOKKLRSMTDKRYRLHLSTADLLFVITLPEFAVDAMNMFNGFLCKAVHVIYTNLYSS 125
OY 124 VLLIAFISDRRLAYIAVHAATNSORPRKILAEKYVYGVWIPALLITPDPFANV-----S 178
DB 126 VLLIAFISDRRLAYIAVHAATNSORPRKILAEKYVYGVWIPALLITPDPFADVSGDLS 185
OY 179 EADDRICRFPNDLVVYVFOFQHIMVGLLPGIYILSCYCIILSKLSHSGHOKRAL 238
DB 186 GQDRIYICDRLPYDSLMMVYVFOFQHIMVGLLPGIYILSCYCIILSKLSHSGHOKRAL 245
OY 239 KTVIILIAFFGCMVLPYVIGISIDSFILLETIKOGCEFNTHKMTISTEALAFHCCGN 298
DB 246 KITVILIAFFGCMVLPYVIGISIDSFILGVRKGGDFESYHKWISTEALAFHCCGN 305
OY 299 PILVAFIAKFKTSQAHLTVSVSGSSLKILSKRGHSGSVSTESESSSFHSS 352
DB 306 PILVAFIAKFKSSAQHAIHNSMRGSSLKILSKRGHSGSVSTESESSSFHSS 359
RESULT 9
ID CCR4_RAT STANDARD: PRT: 349 AA.
AC CCR4_RAT 008565;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR).
GN CXCR4 OR CMKAR4.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MORIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=SPLEEN;
RA HARRISON J.K., SALAFRANCA M.N.;
RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; U90610; G190613; -
DR GCRDB; GCR_1401; -
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7tm_1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
FT DOMAIN 1 36
FT TRANSMEM 37 60
FT DOMAIN 61 76
FT TRANSMEM 77 96
FT DOMAIN 97 107
FT TRANSMEM 108 129
FT DOMAIN 130 151
FT TRANSMEM 152 172
FT DOMAIN 173 197
FT TRANSMEM 198 217
FT DOMAIN 218 237
FT TRANSMEM 238 258
FT DOMAIN 259 282
FT TRANSMEM 283 302
FT DOMAIN 303 349
FT DISULFID 106 183
FT CARBOHYD 8 8

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DR EMBL; X85740; G971452; -
DR GCRDB; GCR 2115; -
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7tm_1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
FT DOMAIN 1 39
FT TRANSMEM 40 67
FT DOMAIN 68 77
FT TRANSMEM 78 98
FT DOMAIN 99 111
FT TRANSMEM 112 133
FT DOMAIN 134 150
FT TRANSMEM 151 175
FT DOMAIN 176 206
FT TRANSMEM 207 226
FT DOMAIN 227 242
FT TRANSMEM 243 267
FT DOMAIN 268 284
FT TRANSMEM 285 308
FT DOMAIN 309 360
FT CARBOHYD 183 183
FT CARBOHYD 194 194
FT DISULFID 110 187
SQ SEQUENCE 360 AA; 41402 MW; 8738E75E CRC32;

Query Match 32.8%; Score 600.5; DB 1; Length 360;
Best Local Similarity 39.7%; Pred. No. 3.1e-34;
Matches 116; Conservative 60; Mismatches 113; Indels 3; Gaps 2;

OY 21 YDSKKEPCFRENANFNKIFLPTISITIFLGIYVNGVLIVMGOKLRSTDKRYRL 80
DB 22 YESIPKPTKGIAFGELFPLPLSLVFGLGNSVYLVLFYKKLRSTMDVYLLNTL 81
OY 81 SVADLLEVTPEFMAVDVAVMVEFGLCKAVHYVTNLSSVLLAFISDRYLAIVH 140
DB 82 AISDLLEFSLPFGMYADQWVGLGCKMISMYLVGFSGIFPVALMSIDRLAIVH 141
OY 141 ATNSQRPKLLAEKVYVGVWIPALLTIPDFIFANVSEADRYICDRFPY--NDLWVY 198
DB 142 AVFSLRATLTLYGYITSLATWSAVFASLPGLFSTCYTERNHTYCKTKYSLNSTMKVL 201
OY 199 FQFQHIWVGLPGVILVSCYCIISKSHSGKHKRAKATTVLLILAFACMPPYIG 258
DB 202 SLENTNIGLVIPGIMFCYSMTIRLQHKNEKKNNAVMTFAVVVLFGLFWTPYIV 261
OY 259 ISIDSFILLEIKOGCEPENTVHKWISTEALAEFHCLNPLVLAFLGAKRK 310
DB 262 LLEFLVELVL-QDCPTEFLDYALQATETLAFHCCLNLIYFFLGKRR 312

RESULT 12
ILRB_RAT STANDARD: PRT: 359 AA.
AC P35407;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA
DE RECEPTOR).
GN ILRB OR CXCR2.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MORIDAE; MURINAE; RATTUS.

RM [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGE-DAMLEY; TISSUE-LUNG;
RA GOEL A.E., WANG S., ZHOU Y., OEBERG K.;
RL SUBMITTED (FEB-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
RM [2]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE-LIVER;
RA KONISHI K., SHIBATA F., MATANABE K., TSURUFUJI S., NAKAGAWA H.,
RA FUJIOKA M.;
RL SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RM [3]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE-SPLEEN, AND LUNG;
RX MEDLINE; 97115810.
RA DUNSTAN C.-A.N., SALAFRANCA M.N., ADHIRARI S., XIA Y., FENG L.,
RA HARRISON J.K.;
RL *Identification of two rat genes orthologous to the human
interleukin-8 receptors*;
RL J. BIOL. CHEM. 271:32770-32776(1996).
CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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DR EMBL; X77797; G498703; -
DR EMBL; D63584; G944819; -
DR EMBL; U70988; G167613; -
DR PIR; S42096; S42096.
DR GCRDB; GCR 0913; -
DR GCRDB; GCR 1405; -
DR GCRDB; GCR 1524; -
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7tm_1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
FT DOMAIN 1 47
FT TRANSMEM 48 74
FT DOMAIN 75 83
FT TRANSMEM 84 104
FT DOMAIN 105 119
FT TRANSMEM 120 141
FT DOMAIN 142 162
FT TRANSMEM 163 182
FT DOMAIN 183 207
FT TRANSMEM 208 230
FT DOMAIN 231 250
FT TRANSMEM 251 272
FT DOMAIN 273 296
FT TRANSMEM 297 314
FT DOMAIN 315 359
FT CARBOHYD 8 8
FT CARBOHYD 23 23
FT CARBOHYD 201 201
FT CARBOHYD 202 202
FT DISULFID 118 195
SQ SEQUENCE 359 AA; 40532 MW; 5B29D194 CRC32;

Query Match 31.8%; Score 581.5; DB 1; Length 359;
Best Local Similarity 36.6%; Pred. No. 6.1e-33;

	Matches	132; Conservative	68; Mismatches	128; Indels	33; Gaps	10
OY	10	DNYT-EMMSGGYDSK-----	EPCCREMANFKFLFTTYSIITLTIVGN	56		
Db	7	DNFSLEDFSGIDISYNSDDPEFTLSDAPC-PSANLIDINRAVVYIVYLTLLSLVGN	65			
OY	57	GLVILVMGQOKRLSMTKDYRLHLVADLLFTTPEFMVADAVANNYFGNGLCKAAHVIT	116			
Db	66	SLVMLVILYNRSTCSYTDVYLLNLALADLFALLTEPMVAAKNYNGIIFSGFLCKVYSFLD	125			
OY	117	TVNLVSYVLLIAFISLDRLAIVHATNSORPKRLAEKVVYVGSWIPALLTITPDEIFAN	176			
Db	126	ELTFYSSVLLLACISMDRFLAIVHATSTLIQKHLV-KFCVIMMPELSIVLSPIFLIRT	184			
OY	177	VSEAD-DRICORFPYN-----DLMVYVQFOHIMGILLPGVILISCTCIISKSLSHK	230			
Db	185	TVKANSTVVC--YENIGNNTSKMWTVAIRLLPQTYGFLPLILMFCYGFITRTLTFFKAN	241			
OY	231	GHOQRKRLKTTVILILAFACMLPYRIGISIDSEFILLEITIKOCCEPENVHKWISTEAL	290			
Db	242	MOGRKRAMVIVIAVVLVFLCMLPIYIVLFTDILMTKLIKKECEQONENKNALEMTETIL	301			
OY	291	AEFHCCLANPILYAFLGAKFKTSAQHALTSVSRGSSKLILSK--GRRGHSVSTSESS	347			
Db	302	GLHSLCLNPIIYAFIGQKFR---HGLLRIM--ANYGLVSKFEPLAKEGRPSFVGSSAMT	355			
OY	348	S 348				
Db	356	S 356				

RESULT	13			
CCRS_HUMAN	STANDARD:	PRT:	368	AA.
AC	P49682.			
DT	01-FEB-1996 (REL. 33, CREATED)			
DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)			
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)			
DE	C-X-C CHEMOKINE RECEPTOR TYPE 3 (CXCR-3) (CXCR-3).			
GN	CXCR3 OR GPR9.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUAROTIA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;			
CC	PRIMATES; CATARRHINI; HOMINIDAE; HOMO.			
LN	(1)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BLOOD.			
RX	MEDLINE: 97188912.			
RA	LOETSCHER M., GERBER B., LOETSCHER P., JONES S.A., PILLI L.,			
RA	CLARK-LEWIS I., BAGGIOLINI M., MOSER B.;			
RT	"Chemokine receptor specific for IP10 and mig: structure, function,			
RL	and expression in activated T-lymphocytes.";			
RN	J. EXP. MED. 184:963-969(1996).			
RN	[2]			
RP	SEQUENCE OE 5-368 FROM N.A.			
RX	MEDLINE: 96115583.			
RA	MARCHESE A., HEIDER M., NGUYEN T., HENG H.H.Q., SALLIYA V.R.,			
RA	CHENG R., MORPH P.M., TSUI L.-C., SHI X., GREGOR P., GEORGE S.R.,			
RT	"Cloning and chromosomal mapping of three novel genes, GPR9, GPR10,			
RT	and GPR14, encoding receptors related to interleukin 8, neuropeptide			
RL	Y, and somatostatin receptors.";			
RL	GENOMICS 29:335-344(1995).			
CC	-1- FUNCTION: RECEPTOR FOR IP10 AND MIG.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/).			
CC	or send an email to license@isb-sib.ch).			

[illegible]

	Query Match	31.5%;	Score 576.5;	DB 1;	Length 368;	
	Best Local Similarity	35.0%;	Pred. No. 1.4e-32;			
	Matches 121;	Conservative	70;	Mismatches 140;	Indels 15;	Gaps 4;
QY	10 DNYTEEMSGSDYS----	MKEPCFEENANFNKIFLPTIYSIIPLTGIIVNGLVILVMGY	65			
	:::::	:::::	:::::			
Dd	21 ENFSSSYDYGENESDSCCTSPCPQDFSLNDRPALFYLSLLFLGLGNCAVAALLS	80				
	:::::	:::::	:::::			
QY	66 QKKLRSMIDKRLHLSVADLLFVITLPWMAVDAAVANNFTGNNFLCAAHVITYVNISYL	125				
	:::::	:::::	:::::			
Dd	81 RRTALSTSDTFLEHLHAVDLTVLTLPMAVDAAVOWFGSLCFAAGAFINIFYAAL	140				
	:::::	:::::	:::::			
QY	126 ILAFISLDTRYAIYHATINSORPRKLAEKVYGVGWIPALLITTPDF--ANVSEADR	183				
	:::::	:::::	:::::			
Dd	141 LLACISPEFRLYNIYHATLYRRGPARYTLICLAWMGCCLFALPDFLFLSAHHDRLNA	200				
	:::::	:::::	:::::			
QY	184 YICREYPNDLMVVVFQFIIMVGILLPGIYILSCYCIISKLSHKGHOKRKALKTYI	243				
	:::::	:::::	:::::			
Dd	201 THCOYNFP-OVGRTALRYLGVLGAGLIELVMACYAHIIIAVLVSROGRRLRARLVVV	259				
	:::::	:::::	:::::			
QY	244 LILAFCNQMLYYIGISIDSFILEIKKGCEFFETVAKWISTFALAFFHCCLNPILYA	303				
	:::::	:::::	:::::			
Dd	260 VVAVFALCWITPETHLVLDLIMDLGALARNCGRSRVDVAVSVTSGLDIYMCCNLPLEYA	319				
	:::::	:::::	:::::			
QY	304 FLGAKFKTSAOHALTSVSRGSKLKLSKGRGSHSVSTESESSEF	349				
	:::::	:::::	:::::			
Dd	320 FVGVKFERRMMLL-----LRLGCGNONGIQROPSSSRKRDSSW	357				
	:::::	:::::	:::::			
RESULT 14						
IL8B_HUMAN	IL8B_HUMAN	STANDARD;	PRT; 360 AA.			
AC	P25025;					
DT	01-MAY-1996 (REL. 22, CREATED)					
DT	01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)					
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)					
DE	HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA RECEPTOR) (IL-8 RECEPTOR TYPE 2).					
DE	IL8RB OR CXCR2.					
GN	HOMO SAPIENS (HUMAN).					
OC	EUKAROTIA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;					
OC	PRIMATE; CATARRHINI; HOMINIDAE; HOMO.					
NN	[1]					

RP SEQUENCE FROM N.A.
 RX MEDLINE: 91368200.
 RA MURPHY P.M., TIFFANY H.L.:
 RT "Cloning of complementary DNA encoding a functional human
 RT Interleukin-8 receptor.";
 RL SCIENCE 253:1280-1283(1991).
 RN [2]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE: 93205012.
 RA CERRETTI D.P., KOZLOSKY C.J., VANDEN BOS T., NELSON N., GEARING D.P.,
 RA BECKMANN M.P.:
 RT "Molecular characterization of receptors for human interleukin-8,
 RT GRO/melanoma growth-stimulatory activity and neutrophil activating
 RT peptide-2.";
 RL MOL. IMMUNOL. 30:359-367(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94209273.
 RA SPRENGER H., LLOYD A.R., LAURENS L.L., BONNER T.I., KELVIN D.J.:
 RT "Structure, genomic organization, and expression of the human
 RT Interleukin-8 receptor B gene.";
 RL J. BIOL. CHEM. 269:11065-11072(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX TISSUE-PLACENTA:
 RX MEDLINE: 95014476.
 RA AHUJA S.K., SHETTY A., TIFFANY H.L., MURPHY P.M.:
 RT "Comparison of the genomic organization and promoter function for
 RT human Interleukin-8 receptors A and B.";
 RL J. BIOL. CHEM. 269:26381-26389(1994).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE: 92355587.
 RA LEE J., HORUK R., RICE G.C., BENNETT G.L., CAMERATO T., WOOD W.I.:
 RT "Characterization of two high affinity human Interleukin-8
 RT receptors.";
 RL J. BIOL. CHEM. 267:16283-16287(1992).
 CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSNGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
 CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M73969; G1109691; -
 DR EMBL: M94582; G186378; -
 DR EMBL: M99412; G576679; -
 DR EMBL: L19593; G559054; -
 DR EMBL: U11869; G511803; -
 DR PIR: A39446; A39446; -
 DR PIR: A53611; A53611; -
 DR GCRDB: GCR_0077; -
 DR GCRDB: GCR_0610; -
 DR GCRDB: GCR_1001; -
 DR GCRDB: GCR_1339; -
 DR GCRDB: GCR_1831; -
 DR MIM: 146928; -
 DR PROSITE: PS00237; G-PROTEIN-RECEPTOR; 1.
 DR PFAM: PF00001; 7tm_1; 1.
 DR HSSP: P34996; 1DDU.
 KM G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 KW CHEMOTAXIS.
 FT DOMAIN 1 48 EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	49	75	1 (POTENTIAL).
FT	DOMAIN	76	84	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	85	105	2 (POTENTIAL).
FT	DOMAIN	106	120	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	121	142	3 (POTENTIAL).
FT	DOMAIN	143	163	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	164	183	4 (POTENTIAL).
FT	DOMAIN	184	208	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	209	231	5 (POTENTIAL).
FT	DOMAIN	232	251	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	252	273	6 (POTENTIAL).
FT	DOMAIN	274	294	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	295	315	7 (POTENTIAL).
FT	DOMAIN	316	360	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	22	22	POTENTIAL.
FT	DISULFID	119	196	BY SIMILARITY.
SO	SEQUENCE	360 AA;	40759 MW;	135SECEAE CRC32.

Query Match 31.08; Score 568; DB 1; Length 360;
 Best Local Similarity 35.34; Pred. No. 5e-32;
 Matches 132; Conservative 69; Mismatches 119; Indels 54; Gaps 11;

QY	9 SDNYT-----EMSGGDYDSM-----KEPCFREANFNKIFLPITYSTIFLGIYGN 56
DB	8 SDSFEDFWKGEDLSNYSSTLPPLLDAAPC-EPSELEIKYVITVALVFLSLIGN 66
QY	57 GLVILVNGYOKRLSMTRDKYRLHLSVADLFLVITLPPFMAVAVANWYGFNLCAVAVIY 116
DB	67 SLVVLVILYSRVSQSVTDVYLNLALADLLFALFLPIMASKVANGWIFGFLCAVVSILK 126
QY	117 TVNLYSSVLIATFSDRYATVATNSQPRKLAERKVVYGVVITALLITIDPIF-- 175
DB	127 EVNYSGLILACISVRYATVATRTLTQKRLV-KFICLSIWGLSLALAPVLLFRR 185
QY	175 ----ANYSEADRYICRFYPNDL--WVVFQFQIHWGLIPGVILUSCYCLISKLSH 228
DB	186 TVYSNNVSPA-----CEDMNNTNANKMLRLILPQSGFVPLIMLFCGFLRLFLK 240
QY	229 SKGHQKRAKLTIVLILAFACWLPYIGISIDSIFLEIINOGCEFEVTHKMSITE 288
DB	241 AHMQCKRAMVIAVAVVFLFLCWLPRNVLLADTLRTQYICQTCRRNHIDRALDATE 300
QY	289 ALAFHCCNLPIATFAGARFKTSNQAHLVSNGSSIKLISKRGRGHSSVTE--- 345
DB	301 ILGLHSCNLNPLIATFAGQFR---HGL-----LKLILAI-----HGLISKSDLPKD 343
QY	345 -----ESSSFHSS 352
DB	344 SRPSFVSSSGHTS 357

RESULT 15
 IL8B_MACMU
 ID IL8B_MACMU STANDARD; PRT; 353 AA.
 AC 028519;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (FRAGMENT).
 GN IL8B OR CXCR2.
 OS MACACA MULATTA (RHESUS MACAQUE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; CERCOPITHECIDAE; CERCOPITHECINAE; MACACA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96175151.
 RA ALVAREZ V., CORO E., SETIEN F., GONZALEZ S., GONZALEZ-RODAS S.,
 RA LOPEZ-LARREA C.:
 RT "Characterization of interleukin-8 receptors in non-human primates.";
 RL IMMUNOGENTICS 43:261-267(1996).
 CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR

Search completed: September 14, 1999, 09:52:44
Job time: 22 sec

CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.

-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

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or send an email to license@isb-sib.ch).

DR EMBL, X91116; E198176; -
DR PROSITE, PS00237; G_PROTEIN_RECEPTOR; 1.
DR PFAM, PF00001; 7tm_1; 1.
DR HSSP, P34996; 1DDO.

DR G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW CHEMOTAXIS.

FT NON_TER 1 1
FT DOMAIN <1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 46 72 1 (POTENTIAL).
FT DOMAIN 73 81 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 82 102 2 (POTENTIAL).
FT DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 118 139 3 (POTENTIAL).
FT DOMAIN 140 160 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 161 180 4 (POTENTIAL).
FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 228 5 (POTENTIAL).
FT DOMAIN 229 248 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 249 270 6 (POTENTIAL).
FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 292 312 7 (POTENTIAL).
FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
FT DISULFID 116 193 BY SIMILARITY.
FT CARBOHYD 19 19 POTENTIAL.
FT NON_TER 353 353
SQ SEQUENCE 353 AA; 39947 MW; B592FE64 CRC32;

Query Match 31.0%; Score 567; DB 1; Length 353;
Best Local Similarity 37.0%; Pred. No. 5,7e-32;
Matches 127; Conservative 64; Mismatches 110; Indels 42; Gaps 9;

OY 27 PCFREANFNKIFLPTIYSILFLGIVNGLVILVMGYOKRLRSMTDKYRLHLVADLL 86
DB 35 PC-RESELEINKYFVYIYALVFLSLGNSLVMYIYSRVGRSVTDVYLLNLALADLL 93
OY 87 FYITLPEFNAVDAVAMWYFENFLCKAVHYIYTNLYSSVLLAFISIDRYLAIVHATNSOR 146
DB 94 FALTLPIMWASKVNGWIFGTFLCKVYSLKEVYFSGILLACISVDRYLAIVHATRIILT 153
OY 147 PKLLAEKVYVGVWIPALLFTIPDFIF-----ANVSEADDRYICDRFPNDL--WVVV 198
DB 154 OKRYLV-KFICSLINGSLILLALPVILFRITYSSNVSPA-----CYEDGNNTANWRRL 207
OY 199 FOFOHIMWGLIPGIVILSCYCIISLSHSGHOKRKALKTTVILILAFACWLPPYITG 258
DB 208 LRLPQSGFVIYPLILMFCYGFILTLFKAHMGQKRAMRYFAVVLFLCWLPLYSIV 267
OY 259 ISIDSFILLEITIKQCEFEFNTVHKWISTEALAFHCCINPLIYAFGLAKFKTSQOHALT 318
DB 268 LLAIDLIRQVIOECERNRNHIDRALDATEILGILHSCINPLIYAFIGOKFR---HGL- 323
OY 319 SVSRGSSLKILSKGKRGHSVSTES-----ESSSPFS 351
DB 323 -----LKILAI-----HGLISKDSLPKDSRPSFVGSSSGHT 353

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 14, 1999, 09:51:02 : Search time 11.24 Seconds

(Without alignments)
1254.720 Million cell updates/sec

Title: US-09-104-063-4

Perfect score: 1830

Sequence: 1 MEGISITSDNYTEMGSGD.....KRGCHSSSVTSESSSFHSS 352

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database: PIR60:*

1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1830	100.0	352	2	A45747	neuropeptide Y/pep
2	1806	98.7	352	2	G00048	fusin (LESTRA) - c
3	1722.5	94.1	353	2	S28787	neuropeptide Y/pep
4	600.5	32.8	360	2	A57160	chemokine (C-C) re
5	582	31.8	367	2	JE0349	interferon-inducib
6	568	31.0	360	2	A53611	interleukin-8 rece
7	567	31.0	356	2	S42096	interleukin-8 rece
8	564.5	30.8	360	2	JC4587	chemokine (C-C) re
9	564	30.8	355	2	QJ1231	interleukin-8 rece
10	563	30.8	378	2	A57355	G protein-coupled
11	559.5	30.6	350	2	A39445	interleukin-8 rece
12	558	30.5	358	2	A53752	interleukin-8 rece
13	557	30.4	378	2	B55735	lymphocyte-specifi
14	549.5	30.0	355	2	JC4304	orphan G-protein-c
15	544	29.7	327	2	S56162	MOCKR15 protein - h
16	540	29.5	372	2	S26667	G protein-coupled
17	539	29.5	359	2	A48921	interleukin-8 rece
18	538	29.4	378	2	A45680	G protein-coupled
19	536	29.3	374	2	S42658	G protein-coupled
20	533.5	29.2	369	2	JC5068	G protein-coupled
21	529	28.9	374	2	S2785	G protein-coupled
22	528	28.9	374	2	I38450	chemokine (C-C) re
23	527	28.8	355	2	JC5067	G protein-coupled
24	519.5	28.4	383	2	S55594	G protein-coupled
25	514.5	28.1	354	2	I58186	hypothetical G-pro
26	512.5	28.0	360	2	JC2443	chemokine (C-C) re
27	509	27.8	355	2	G02436	C-C chemokine rece
28	507	27.7	355	2	A57237	chemokine (C-C) re
29	506	27.7	352	2	A43113	chemokine (C-C) re
30	503.5	27.5	355	2	A45177	chemokine (C-C) re
31	502.5	27.5	359	2	S15403	angiotensin II rec
32	501.5	27.4	350	2	JN0621	G-protein coupled
33	493.5	27.0	359	2	JC1104	angiotensin II rec
34	493.5	27.0	359	2	A42656	angiotensin II rec
35	488.5	26.7	359	2	S44425	angiotensin II rec
36	487.5	26.6	359	2	J01516	angiotensin II rec
37	485	26.5	362	2	JN0694	angiotensin II rec
38	484.5	26.5	359	2	A48857	Angiotensin II rec
39	483.5	26.4	359	2	JH0621	angiotensin II rec

40	481	26.3	359	2	I49341	MIP-1 alpha recept
41	480.5	26.3	359	2	JC2134	angiotensin II rec
42	474.5	25.9	359	2	I39418	angiotensin II typ
43	473.5	25.9	362	2	A30341	G protein-coupled
44	473	25.8	359	2	JC1193	angiotensin II rec
45	472.5	25.8	359	2	JC1194	angiotensin II rec

ALIGNMENTS

RESULT 1

A45747

neuropeptide Y/peptide YY receptor Y3 - human

N:Alternate names: fusin; H89; leukocyte-derived seven-transmembrane receptor LESTR;

C:Species: Homo sapiens (man)

C:Date: 03-May-1994 #sequence revision 03-May-1994 #text change 17-Mar-1999

C:Accession: A45747; A53103; I53006; I59444; I69203; S32761

R:Feederpiel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-L

Genomics 16, 707-712, 1993

A:Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a

A:Reference number: A45747; MUID:93315164

A:Accession: A45747

A:Molecule type: mRNA

A:Residues: 1-352 <FEED>

A:Cross-references: GB:M9293; NID:g292516; PID:g292517

R:Loetscher, M.; Geisler, T.; O'Reilly, T.; Zwaalen, R.; Baggiolini, M.; Moser, B.

J. Biol. Chem. 269, 232-237, 1994

A:Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highl

A:Reference number: A53103; MUID:94103215

A:Accession: A53103

A:Molecule type: mRNA

A:Residues: 1-352 <LOE>

A:Cross-references: EMBL:X71635; NID:g297099; PID:g297100

R:Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.

DNA Cell Biol. 12, 465-471, 1993

A:Title: Molecular cloning, characterization, and localization of the human homolog t

A:Reference number: I53006; MUID:93319629

A:Accession: I53006

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-352 <HER>

A:Cross-references: GB:L06797; NID:g414929; PID:g414928

R:Jazin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salton, J.

Regul. Pept. 47, 247-258, 1993

A:Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human hom

A:Reference number: I59444; MUID:94052833

A:Accession: I59444

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-352 <RES>

A:Cross-references: GB:D10924; NID:g219868; PID:g219869

C:Genetics:

A:Gene: GDB:NPY3R; NPY3

A:Cross-references: GDB:230002; OMIM:162643

A:Map position: 2q21.2q21

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 100.0%; Score 1830; DB 2; Length 352;

Best Local Similarity 100.0%; Pred. No. 4.6e-143; Indels 0; Gaps 0;

Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MEGISITSDNYTEMGSGDYSKKEPCFRENNFNKIFLPTIYSIIIFLTGIVGNGLVI 60

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Db      1  MEGISITSDNTYEEEMSGSDYDSMKKEPCFEENANFNKIFLPTIYSITFLTGIVNGLYI 60
QY      61  LVNGYQKRLRSMTDKYRLHLVSADLLFVITLPEWAVDAVANWYFGNPLCKAVHIYTVNL 120
Db      61  LVNGYQKRLRSMTDKYRLHLVSADLLFVITLPEWAVDAVANWYFGNPLCKAVHIYTVNL 120
QY      121 YSSVLLAFISLDRIYLAIVATNSQRPRLKLAERKVVYGVWIPALLITPDIFFANVSEA 180
Db      121 YSSVLLAFISLDRIYLAIVATNSQRPRLKLAERKVVYGVWIPALLITPDIFFANVSEA 180
QY      181 DDRYICDRFPNDLWVYVFOFHIMVGLIPGIVILSCYCIITISKLSHGQRKALKT 240
Db      181 DDRYICDRFPNDLWVYVFOFHIMVGLIPGIVILSCYCIITISKLSHGQRKALKT 240
QY      241 TVLLIAFFACWLPYYIGISIDSFILLEIKQCEFEENTVHKMISTEALAFPHCCINPI 300
Db      241 TVLLIAFFACWLPYYIGISIDSFILLEIKQCEFEENTVHKMISTEALAFPHCCINPI 300
QY      301 LVAFLEAKFKTSQHALTYSRSGSSLKILSKGRGHSSTESSESSFHSS 352
Db      301 LVAFLEAKFKTSQHALTYSRSGSSLKILSKGRGHSSTESSESSFHSS 352

```

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RESULT 2
G00048
fusion (LESTRA) - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 11-Apr-1997
C:Accession: G00048
R:Atsumi, M.
submitted to GenBank, July 1996
A:Reference number: H00048
A:Accession: G00048
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-352 <TA1>
A:Cross-references: GB:D86579; NID:g1468948; PID:g1468949

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Query Match          98.7%; Score 1806; DB 2; Length 352;
Best Local Similarity 98.3%; Pred. No. 4.3e-141;
Matches 346; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

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QY      1  MEGISITSDNTYEEEMSGSDYDSMKKEPCFEENANFNKIFLPTIYSITFLTGIVNGLYI 60
Db      1  MEGISITSDNTYEEEMSGSDYDSMKKEPCFEENANFNKIFLPTIYSITFLTGIVNGLYI 60
QY      61  LVNGYQKRLRSMTDKYRLHLVSADLLFVITLPEWAVDAVANWYFGNPLCKAVHIYTVNL 120
Db      61  LVNGYQKRLRSMTDKYRLHLVSADLLFVITLPEWAVDAVANWYFGNPLCKAVHIYTVNL 120
QY      121 YSSVLLAFISLDRIYLAIVATNSQRPRLKLAERKVVYGVWIPALLITPDIFFANVSEA 180
Db      121 YSSVLLAFISLDRIYLAIVATNSQRPRLKLAERKVVYGVWIPALLITPDIFFANVSEA 180
QY      181 DDRYICDRFPNDLWVYVFOFHIMVGLIPGIVILSCYCIITISKLSHGQRKALKT 240
Db      181 DDRYICDRFPNDLWVYVFOFHIMVGLIPGIVILSCYCIITISKLSHGQRKALKT 240
QY      241 TVLLIAFFACWLPYYIGISIDSFILLEIKQCEFEENTVHKMISTEALAFPHCCINPI 300
Db      241 TVLLIAFFACWLPYYIGISIDSFILLEIKQCEFEENTVHKMISTEALAFPHCCINPI 300
QY      301 LVAFLEAKFKTSQHALTYSRSGSSLKILSKGRGHSSTESSESSFHSS 352
Db      301 LVAFLEAKFKTSQHALTYSRSGSSLKILSKGRGHSSTESSESSFHSS 352

```

```

RESULT 3
S28787
neuropeptide Y/peptide YY receptor Y3 - bovine
C:Species: Bos primigenius taurus (cattle)

```

```

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 06-Dec-1996
C:Accession: S28787
R:Rimland, J.; Xin, W.; Sweetnam, P.; Saljoh, K.; Nestler, E.J.; Duman, R.S.
Mol. Pharmacol. 40, 869-875, 1991
A>Title: Sequence and expression of a neuropeptide Y receptor cDNA.
A:Reference number: S28787; MUID:92100053
A:Accession: S28787
A:Molecule type: mRNA
A:Residues: 1-353 <RIM>
A:Cross-references: EMBL:M86739
C:Keywords: appetite; G protein-coupled receptor; transmembrane protein

```

```

Query Match          94.1%; Score 1722.5; DB 2; Length 353;
Best Local Similarity 92.4%; Pred. No. 3.1e-134;
Matches 326; Conservative 20; Mismatches 6; Indels 1; Gaps 1;

```

```

QY      1  MEGISITSDNTYE-EMSGSDYDSMKKEPCFEENANFNKIFLPTIYSITFLTGIVNGLYI 59
Db      1  MEGIRIFTDNTTDDDLGSDYDSMKKEPCFEENANFNKIFLPTIYSITFLTGIVNGLYI 60
QY      60  LVNGYQKRLRSMTDKYRLHLVSADLLFVITLPEWAVDAVANWYFGNPLCKAVHIYTVN 119
Db      61  LVNGYQKRLRSMTDKYRLHLVSADLLFVITLPEWAVDAVANWYFGNPLCKAVHIYTVN 120
QY      120 LVSSVLLAFISLDRIYLAIVATNSQRPRLKLAERKVVYGVWIPALLITPDIFFANVSE 179
Db      121 LVSSVLLAFISLDRIYLAIVATNSQRPRLKLAERKVVYGVWIPALLITPDIFFADIKE 180
QY      180 ADDRYICDRFPNDLWVYVFOFHIMVGLIPGIVILSCYCIITISKLSHGQRKALK 239
Db      181 VDRYICDRFPNDLWVYVFOFHIMVGLIPGIVILSCYCIITISKLSHGQRKALK 240
QY      240 TVYLLIAFFACWLPYYIGISIDSFILLEIKQCEFEENTVHKMISTEALAFPHCCINP 299
Db      241 TVYLLIAFFACWLPYYIGISIDSFILLEIKQCEFEENTVHKMISTEALAFPHCCINP 300
QY      300 LVAFLEAKFKTSQHALTYSRSGSSLKILSKGRGHSSTESSESSFHSS 352
Db      301 LVAFLEAKFKTSQHALTYSRSGSSLKILSKGRGHSSTESSESSFHSS 353

```

```

RESULT 4
A57160
chemokine (C-C) receptor 4 - human
N:Alternate names: C-C CKR-4
C:Species: Homo sapiens (man)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: A57160
R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.
J. Biol. Chem. 270, 19495-19500, 1995
A>Title: Molecular cloning and functional expression of a novel CC chemokine receptor
A:Reference number: A57160; MUID:95370289
A:Accession: A57160
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-360 <POW>
A:Cross-references: GB:X85740; NID:g1370103; PID:g9711452
A:Note: source clone K5-5
C:Genetics:
A:Gene: GDB:CMKBR4
A:Cross-references: GDB:677463
A:Map position: 3p21-3p21
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
F:40-65/Domain: transmembrane #status predicted <TM1>
F:76-97/Domain: transmembrane #status predicted <TM2>
F:112-133/Domain: transmembrane #status predicted <TM3>
F:151-175/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:243-264/Domain: transmembrane #status predicted <TM6>
F:291-308/Domain: transmembrane #status predicted <TM7>
F:229-276,110-187/Disulfide bonds: #status predicted
F:72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predi

```

F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F:183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

```

Query Match          32.8%; Score 600.5; DB 2; Length 360;
Best Local Similarity 39.7%; Pred. No. 3,7e-42;
Matches 116; Conservative 60; Mismatches 113; Indels 3; Gaps 2;

QY 21 YSMKEPCREENANFNKIFLPTIYSIFLTGIVNGVILVNGYOKLRSMTRYLHL 80
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 22 YSIPKPCKEGKARGEFLPLPLYSFLVFGLGNSVVLVLFKKRLRSMTRYLNL 81

QY 81 SVADLFVLTLPMAVDAAVNWEGNLFCKAVHVTIVNLYSSVLLAFISDRYLAIV 140
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 82 AISDLFLVSLFSPMGYAADQWFGGLCKMISMWLVGFSIFVMSIDRYLAIV 141

QY 141 ATNSQRPRLAEKVVYVGMIPALLTIPDFIFANVSEADRYICDRFP--NDLWVY 198
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 AVFSLSARLTITGVITSLATMSVAVFASLPGFLSTCYERNITTKTKYSLNSTWKYL 201

QY 199 FQFQHMVGLLPGVILSCYCIISKLSHSGHQRKALKTTVIIILAFACWLPYIG 258
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 202 SSLEINILGLVPLGIMLECYSMIIRTLQCKNEKNKAKMIFAVYVFLGFWPTYNIV 261

QY 259 ISIDSFILLEIKQCEFNVTWKWISITELAFPHCCNPLIYAFGLAKK 310
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 262 LPELTIVELVL-QDCTFERIYDAIQAETTLTAFVHCCLNPIYFLGKKR 312
  
```

```

RESULT 5
JE0349
Interferon-inducible protein 10 (IP-10) receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Feb-1999 #sequence-revision 05-Feb-1999 #text-change 05-Feb-1999
C:Accession: JE0349
R:Tamariu, M.; Tomlinaga, Y.; Yatsunami, K.; Narumi, S.
Biochem. Biophys. Res. Commun. 251, 41-48, 1998
A:Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its
A:Reference number: JE0349
A:Accession: JE0349
A:Molecule type: mRNA
A:Residues: 1-367 <TAM>
A:Cross-references: DDBJ:AB003174
C:Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
  
```

```

Query Match          31.8%; Score 582; DB 2; Length 367;
Best Local Similarity 35.6%; Pred. No. 1.2e-40;
Matches 121; Conservative 70; Mismatches 133; Indels 16; Gaps 6;

QY 15 EMGSGDYD-SMKEPCREENANFNKIFLPTIYSIFLTGIVNGVILVNGYOKLRSM 73
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 28 DVGENSEDSPPCPQDPSLNFDRFLPALYSFLFLILGLGAAVAALLSQRLAST 87

QY 74 DKYRLHLSVADLLEFVITLFPMAVDAAVNWYFGNLFCKAVHVTIVNLYSSVLLAFIS 133
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 88 DFFLLHLAVADVLLVTLTFLMAVDAAVQWVFGGLCKVAGALENINIFYAGAPLLACIS 147

QY 134 RLTAIVHATNSQR--PRKLAEKVVYVGMIPALLTIPDFIF--ANVSEADRYICDRF 189
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 148 RLSTIVHATQIRPDRPRVAV--LLCTIVWAGLCLFALPDFILSYANYDQRLNATHCQYN 205

QY 190 YNDLWVWVVFQFQHMVGLLPGVILSCYCIISKLSHSGHQRKALKTTVIIILAF 249
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 206 FP-QVGRTRLRVLQVAGFLPLLVMAVYCAHLLAVLVSRRGRRRARLVVVVVAARA 264

QY 250 ACWLPYIIGISIDSFILLEIKQCEFNVTWKWISITELAFPHCCNPLIYAFGLAKK 309
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 265 VCMTPYHLVVLVLDMDVGVLANRCGRSHVDYAKSVTSGMGVHCCLNPIYAFGVAF 324

QY 310 KTSAGHALTVSRGSSSLKILSKGRGHSSVSSESSSF 349
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
  
```

Db 325 REQMMLFLRLGRSD-----QKGPONQSSSKRESSW 356

```

RESULT 6
A53611
Interleukin-8 receptor type B - human
C:Species: Homo sapiens (man)
C:Date: 07-Oct-1994 #sequence-revision 12-Apr-1996 #text-change 29-Aug-1997
C:Accession: I37898; I38712; A53611; A39446
R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A:Title: Comparison of the genomic organization and promoter function for human inter
A:Reference number: I37898; MUID:95014476
A:Accession: I37898
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-360 <RES>
A:Cross-references: EMBL:U11869; NID:9511801; PID:9511803
A:Accession: I38712
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15 <RE2>
A:Cross-references: EMBL:U11872; NID:9511808; PID:9511809; EMBL:U11873; NID:9511810;
6; PID:9511817; EMBL:U11877; NID:9511818; PID:9511819; EMBL:U11878; NID:9511820; PID:
J. Biol. Chem. 269, 11065-11072, 1994
A:Title: Structure, genomic organization, and expression of the human interleukin-8
A:Reference number: A53611; MUID:94209273
A:Accession: A53611
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 6-360 <SPR>
A:Cross-references: GB:M99412; GB:L19593
R:Murphy, P.M.; Tiffany, H.L.
Science 253, 1280-1283, 1991
A:Title: Cloning of complementary DNA encoding a functional human interleukin-8 recep
A:Reference number: A39446; MUID:91368200
A:Accession: A39446
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 6-360 <MUR>
A:Cross-references: GB:M73969
A:Cross-references: GB:M73969
C:Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8,
C:Genetics:
A:Gene: GDB:IL8RB; IL8RA
A:Cross-references: GDB:127868; OMIM:146928
A:Map position: 2q35-2q35
C:Keywords: G protein-coupled receptor; transmembrane protein
  
```

```

Query Match          31.0%; Score 568; DB 2; Length 360;
Best Local Similarity 35.3%; Pred. No. 1.7e-39;
Matches 132; Conservative 69; Mismatches 119; Indels 54; Gaps 11;

QY 9 SDNYT-----EMGSGDYDSM-----KEPCREENANFNKIFLPTIYSIFLTGIVN 56
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 SDSFDFWKGEDLSNYSSTLPPFLDLAARCP-ESELEINKFYVITAYLAVFLSLGN 66

QY 57 GLVILVNGYOKLRSMTRYLHLSVADLLEFVITLFPMAVDAAVNWYFGNLFCKAVHVT 116
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 SLVMVILYTSRYRGSVTVDDYLLNLALDLFLATLPIMASKVNMIGTFICKVYSLK 126

QY 117 TVNYSVVLILAFISDRPLAVHATNSQRPRKLAEKVVYVGMIPALLTIPDFIF-- 175
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 127 EYNFSGILLIACISVDRLAIVHATRTLTQKRYIV-KFICLSIGLSLLALPVLFRR 185

QY 175 ---ANVSEADRYICDRFPNDL--VWVVFQFQHMVGLLPGVILVSCYCIISKLSH 228
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 186 TVYSSNVSPA-----CYEDMGNTANMWRLLRLPQSGFIVPLIMFCYFTLRILFK 240

QY 229 SKGHQRKALKTTVILLIAFFACWLPYIIGISIDSFILLEIKQCEFNVTWKWISITE 288
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 241 AHMGOKHRAVRVFAVVLIFLCLWLPYNLVLDADLIMRTOVIOETCERRNHIDRALDATE 300
  
```


Db 62 PKSVTDIYLNLALSDLLFVATLPEFWTHYLINCKGLNNAKCTTAFFIFGFGSIFIT 121
QY 129 FTSLDRLYLVAATNSQRPRLAEKVYVGVWIPALLTIPDFIPANVSEADRYICDR 188
DB 122 VISIDRYLAIVLAANSNNRVTQHGVTISLGWAAAILVAAPQFMFTKOKENE---CLG 177
QY 189 FYP---NDLWVVFQFOHIMVGLIPGIVILSCYCIISKLSKSGHOKRAKATVILI 245
DB 178 DYPEVIGETIPVLRNVTNELGFLPLILNSYCFRIQTLFSCNNKRAKAKITLLV 237
QY 246 LAFFACMLPYIGISIDSEILLETIKOGCEFFENTVHKWISTEALAFHCLNPLIYAF 305
DB 238 IVEFLFMTPTYNWIFLETIKLYDEF-PSCDMRKDLALSVETVAFSHCLNPLIYAF 296
QY 306 GAKFKTSAGHALTSVSGSSKIL-----SKGRGHSYSVSTESSESSPHSS 352
DB 297 GEKFRRLYHLV----GKCLAVLCGRSVHVDPSSESQSRHRGSVL--SSNFTYHTS 347

RESULT 15

S56162
MDCR15 protein - human
C:Species: Homo sapiens (man)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 10-Sep-1997
C:Accession: S56162
R:Barella, L.; Loetscher, M.; Tobler, A.; Baggiolini, M.; Moser, B.
Biochem. J. 309, 773-779, 1995
A:Title: Sequence variation of a novel heptahelical leucocyte receptor through alternat
A:Reference number: S56162
A:Accession: S56162
A:Status: Preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-327 <BAR>
A:Cross-references: EMBL:X68829; NID:g840783; PID:g840784

Query Match 29.7% Score 544; DB 2; Length 327;
Best Local Similarity 34.2% Pred. No. 1,4e-37;
Matches 113; Conservative 70; Mismatches 123; Indels 24; Gaps 4;

QY 34 ANFNKIFLPTISIFLTIVGNGVILVMGYOKLRSMTDKYLRLSVADLLFVITLTPF 93
DB 2 ASFKAVFVPVAISLFLGLGVIGNVLVTLERHRQTRSTETFLFLAVADLLVFIILPF 61
QY 94 WAVDAVAMVYFQNFLLCKAAVYITVNLVSSVLLAFISLDRYLAIVHATNSQRPRLAE 153
DB 62 AVAEGSVGVNLTFLCKTYIALHKVNFYCSSILLACIADVRLAIYHAYHAYRHRRLSI 121
QY 154 KVVYVGVWIPALLTIPDFIPANVSEADRYICDRFPNDLWVVF----- 200
DB 122 HITCGTIWVGLFLLAPELLFAKVSOG-----HHNNSLPRCTFSGENQAEHAFMTS 173
QY 200 QFOHIMVGLIPGIVILSCYCIISKLSKSGH-QKRAKAKTIVILILAFHCLNPLIYAF 258
DB 174 RFLYHVAGFLPLVMVGCYGVVHRLRQARRPQOKAVRAILLVTSIFFLCWSPHYIV 233
QY 259 ISIDSEILLETIKOGCEFFENTVHKWISTEALAFHCLNPLIYAFGAKFKTSAGHALT 318
DB 234 IFLDLARLKAADVNTCKLNGSLPVAITMCEFLGHAHCCLNPLIYTFAGVYKFRSDLSRLIT 293
QY 319 SVSRGSSLKILSKGRGHSYSVSTESSESS 348
DB 294 KLGGTSPASLCOLPSPWRSSLS-ESENAT 322

Search completed: September 14, 1999, 09:51:24
Job time: 22 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 14, 1999, 09:51:02 : Search time 23.15 Seconds
(Without alignments)
864.389 Million cell updates/sec

Title: US-09-104-063-4
1830
Sequence: 1 MEGISITSDNYTDEMGSQD.....KRGHSVSTSESSSFHSS 352

Scoring table: BLOSUM62

Searched: 453288 seqs, 56848278 residues

Database :

Pending Patents, AA:*

1: /cgn2_6/ptodata/2/paa/PCTUS9.COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US07.COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US080.COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US081.COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US082.COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US083.COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US084.COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US084B.COMB.pep.*
9: /cgn2_6/ptodata/2/paa/US085.COMB.pep.*
10: /cgn2_6/ptodata/2/paa/US086.COMB.pep.*
11: /cgn2_6/ptodata/2/paa/US087.COMB.pep.*
12: /cgn2_6/ptodata/2/paa/US088.COMB.pep.*
13: /cgn2_6/ptodata/2/paa/US089.COMB.pep.*
14: /cgn2_6/ptodata/2/paa/US090.COMB.pep.*
15: /cgn2_6/ptodata/2/paa/US091.COMB.pep.*
16: /cgn2_6/ptodata/2/paa/US092.COMB.pep.*
17: /cgn2_6/ptodata/2/paa/US093.COMB.pep.*
18: /cgn2_6/ptodata/2/paa/US60.COMB.pep.*
19: /cgn2_6/ptodata/1/paa/PCT_NEW.COMB.pep.*
20: /cgn2_6/ptodata/1/paa/US07_NEW.COMB.pep.*
21: /cgn2_6/ptodata/1/paa/US08_NEW.COMB.pep.*
22: /cgn2_6/ptodata/1/paa/US09_NEW.COMB.pep.*
23: /cgn2_6/ptodata/1/paa/US60_NEW.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1830	100.0	352	1	PCT-US93-10672-2	Sequence 2, Appl1
2	1830	100.0	352	6	US-08-308-880-2	Sequence 2, Appl1
3	1830	100.0	352	7	US-08-441-562-2	Sequence 2, Appl1
4	1830	100.0	352	12	US-08-801-228-4	Sequence 4, Appl1
5	1830	100.0	352	12	US-08-801-228-4	Sequence 4, Appl1
6	1830	100.0	352	12	US-08-802-627-4	Sequence 4, Appl1
7	1830	100.0	352	12	US-08-802-627-4	Sequence 4, Appl1
8	1830	100.0	352	15	US-09-104-063-4	Sequence 4, Appl1
9	1830	100.0	352	15	US-09-104-296-4	Sequence 4, Appl1
10	1808	98.8	356	15	US-09-122-068-2	Sequence 4, Appl1
11	1789	97.8	352	4	US-08-182-962-6	Sequence 6, Appl1
12	1789	97.8	352	7	US-08-446-669-6	Sequence 6, Appl1
13	1789	97.8	352	7	US-08-450-393-6	Sequence 6, Appl1
14	1752	95.7	337	2	US-07-977-452A-21	Sequence 6, Appl1
15	1752	95.7	337	2	US-08-245-242-46	Sequence 21, Appl1
16	1752	95.7	337	22	US-09-299-843A-46	Sequence 46, Appl1
17	600.5	32.8	360	10	US-08-675-814-14	Sequence 14, Appl1
18	600.5	32.8	360	12	US-08-875-573-20	Sequence 20, Appl1
19	600.5	32.8	360	12	US-08-887-977-16	Sequence 16, Appl1
20	600.5	32.8	360	13	US-08-989-107-34	Sequence 34, Appl1

21	600.5	32.8	360	14	US-09-045-583-55	Sequence 55, Appl1
22	600.5	32.8	360	14	US-09-067-447-34	Sequence 34, Appl1
23	600.5	32.8	360	14	US-09-067-447-34	Sequence 34, Appl1
24	600.5	32.8	360	16	US-09-232-878-2	Sequence 2, Appl1
25	594	32.5	123	9	US-08-513-974B-330	Sequence 330, App
26	588.5	32.2	360	12	US-08-833-752-10	Sequence 10, Appl1
27	576.5	31.5	368	11	US-08-708-838-2	Sequence 2, Appl1
28	576.5	31.5	368	12	US-08-829-839-2	Sequence 2, Appl1
29	568	31.0	355	1	PCT-US93-10672-4	Sequence 4, Appl1
30	568	31.0	353	1	PCT-US96-00499A-9	Sequence 9, Appl1
31	568	31.0	353	4	US-08-182-962-8	Sequence 8, Appl1
32	568	31.0	355	4	US-08-308-880-4	Sequence 4, Appl1
33	568	31.0	355	6	US-08-390-000A-5	Sequence 5, Appl1
34	568	31.0	355	6	US-08-441-562-4	Sequence 4, Appl1
35	568	31.0	355	7	US-08-446-669-8	Sequence 8, Appl1
36	568	31.0	355	7	US-08-450-393-8	Sequence 8, Appl1
37	568	31.0	355	7	US-08-605-185-22	Sequence 22, Appl1
38	568	31.0	360	16	US-09-238-166-4	Sequence 4, Appl1
39	567.5	31.0	415	1	PCT-US96-00499A-2	Sequence 2, Appl1
40	567.5	31.0	415	1	PCT-US96-00499A-2	Sequence 2, Appl1
41	567.5	31.0	415	1	PCT-US96-00499A-2	Sequence 2, Appl1
42	563	30.8	378	5	US-08-245-242-66	Sequence 66, Appl1
43	563	30.8	378	22	US-09-299-843A-66	Sequence 66, Appl1
44	557.5	30.5	350	1	PCT-US93-10672-3	Sequence 3, Appl1
45	557.5	30.5	350	1	PCT-US99-11842-27	Sequence 27, Appl1

ALIGNMENTS

RESULT 1

Sequence 2, Application PC/TUS9310672

GENERAL INFORMATION:

APPLICANT: GENENTECH, INC.

NUMBER OF INVENTIONS: CC-CHEMOKINE RECEPTOR

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/10672

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Pitts, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 806

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1489

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

TOPOLOGY: linear

PCT-US93-10672-2

Query Match 100.0% Score 1830. DB 1: Length 352.

Best Local Similarity 100.0%; Pred. No. 2,1e-167;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 MEGISITSDNTYEMGSGDYDSMKKEPCFREANANKIFLPTIYSITFLGTIVGNGLVI 60
        |||
DB      1 MEGISITSDNTYEMGSGDYDSMKKEPCFREANANKIFLPTIYSITFLGTIVGNGLVI 60
QY      61 LVNGYOKKLKSMYDKYRLHLSTVADLLFVITLPPWADAVANWVFGNLCRAVHYIYVNL 120
        |||
DB      61 LVNGYOKKLKSMYDKYRLHLSTVADLLFVITLPPWADAVANWVFGNLCRAVHYIYVNL 120
QY      121 YSSVLLIAFISLDRLYLAIVAHATNSORPRKLLAEKVYVGVWIPALLLTIDPFIFANSEA 180
        |||
DB      121 YSSVLLIAFISLDRLYLAIVAHATNSORPRKLLAEKVYVGVWIPALLLTIDPFIFANSEA 180
QY      181 DDRYICDRFPNDLWVWVFOFQHMGLIPGIYILSCYCIITISKLSHSGHOKRKALKT 240
        |||
DB      181 DDRYICDRFPNDLWVWVFOFQHMGLIPGIYILSCYCIITISKLSHSGHOKRKALKT 240
QY      241 TVLLILAFACWLPYYIGISIDSFILLEITKOGCEPENTVHKWISTEALAFPCCLNPI 300
        |||
DB      241 TVLLILAFACWLPYYIGISIDSFILLEITKOGCEPENTVHKWISTEALAFPCCLNPI 300
QY      301 LVAFLEAKFRTSAQHALLTSVRGSSSLKILSKRGKSHSVSTSESSSFHSS 352
        |||
DB      301 LVAFLEAKFRTSAQHALLTSVRGSSSLKILSKRGKSHSVSTSESSSFHSS 352

```

RESULT 2

US-08-308-880-2
; Sequence 2, Application US/08308880

GENERAL INFORMATION:

APPLICANT: RICHARD HORUK, KULDEEP NEOTE, THOMAS SCHALL

TITLE OF INVENTION: CC-CHEMOKINE RECEPTOR

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/308,880

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/974025

FILING DATE: 10-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: Fitts, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 806

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1489

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-308-880-2

Query Match 100.0%; Score 1830; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 2,1e-167;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 MEGISITSDNTYEMGSGDYDSMKKEPCFREANANKIFLPTIYSITFLGTIVGNGLVI 60
        |||
DB      1 MEGISITSDNTYEMGSGDYDSMKKEPCFREANANKIFLPTIYSITFLGTIVGNGLVI 60
QY      61 LVNGYOKKLKSMYDKYRLHLSTVADLLFVITLPPWADAVANWVFGNLCRAVHYIYVNL 120
        |||
DB      61 LVNGYOKKLKSMYDKYRLHLSTVADLLFVITLPPWADAVANWVFGNLCRAVHYIYVNL 120
QY      121 YSSVLLIAFISLDRLYLAIVAHATNSORPRKLLAEKVYVGVWIPALLLTIDPFIFANSEA 180
        |||
DB      121 YSSVLLIAFISLDRLYLAIVAHATNSORPRKLLAEKVYVGVWIPALLLTIDPFIFANSEA 180
QY      181 DDRYICDRFPNDLWVWVFOFQHMGLIPGIYILSCYCIITISKLSHSGHOKRKALKT 240
        |||
DB      181 DDRYICDRFPNDLWVWVFOFQHMGLIPGIYILSCYCIITISKLSHSGHOKRKALKT 240
QY      241 TVLLILAFACWLPYYIGISIDSFILLEITKOGCEPENTVHKWISTEALAFPCCLNPI 300
        |||
DB      241 TVLLILAFACWLPYYIGISIDSFILLEITKOGCEPENTVHKWISTEALAFPCCLNPI 300
QY      301 LVAFLEAKFRTSAQHALLTSVRGSSSLKILSKRGKSHSVSTSESSSFHSS 352
        |||
DB      301 LVAFLEAKFRTSAQHALLTSVRGSSSLKILSKRGKSHSVSTSESSSFHSS 352

```

RESULT 3

US-08-441-562-2
; Sequence 2, Application US/08441562

GENERAL INFORMATION:

APPLICANT: RICHARD HORUK, KULDEEP NEOTE, THOMAS SCHALL

TITLE OF INVENTION: Nucleic Acids Encoding C-C Chemokine Receptor

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,562

FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/308880

FILING DATE: 19-SEP-1994

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER: 07/974025

FILING DATE: 10-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P0806C1D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5530

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: Amino Acid

TOPOLOGY: linear

US-08-441-562-2

Query Match 100.0%; Score 1830; DB 7; Length 352;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 2,1e-167;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MEGISITSDNYTEEMSGDYDSMKPCPFRENNANFNKIFLPTIYSIIFLTGIVGNGLVI 60
    |||||||
DB 1 MEGISITSDNYTEEMSGDYDSMKPCPFRENNANFNKIFLPTIYSIIFLTGIVGNGLVI 60
    |||||||
QY 61 LVMGYQKLLSMMDKYRLHLSVADLLFVITLPPFAVADVAVANWYFGNPLCAVAVHYIYVNL 120
    |||||||
DB 61 LVMGYQKLLSMMDKYRLHLSVADLLFVITLPPFAVADVAVANWYFGNPLCAVAVHYIYVNL 120
    |||||||
QY 121 YSSVLLIAFTSLDRYLAIIVATNSQRPRLAEKVVYVGVWIPALLTIPDFIFANVSEA 180
    |||||||
DB 121 YSSVLLIAFTSLDRYLAIIVATNSQRPRLAEKVVYVGVWIPALLTIPDFIFANVSEA 180
    |||||||
QY 181 DDRYICDRFPNDLMVVVFOQIIMVGLLPGIYILSCYCIISKLSHSGHOKRKALKT 240
    |||||||
DB 181 DDRYICDRFPNDLMVVVFOQIIMVGLLPGIYILSCYCIISKLSHSGHOKRKALKT 240
    |||||||
QY 241 TVIIILAFACWLPYYIGISIDSFILLEIIKGCEFEFNTVHKWISTEALAFHCCLNPI 300
    |||||||
DB 241 TVIIILAFACWLPYYIGISIDSFILLEIIKGCEFEFNTVHKWISTEALAFHCCLNPI 300
    |||||||
QY 301 LVAFLLGAKFKFTSAQHALTYSRGSLSKILSKGRGSHSVSTESSESSFHSS 352
    |||||||
DB 301 LVAFLLGAKFKFTSAQHALTYSRGSLSKILSKGRGSHSVSTESSESSFHSS 352
    |||||||

```

RESULT 4
US-08-801-228-4
Sequence 4, Application US/08801228

```

: GENERAL INFORMATION:
: APPLICANT: Lee, James
: TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION OF
: TITLE OF INVENTION: PFA4 RECEPTOR NUCLEIC ACID
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Winpatin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/801,228
: FILING DATE: 19-Feb-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/284586
: FILING DATE: 10-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/076093
: FILING DATE: 11-JUN-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/810782
: FILING DATE: 19-DEC-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: P0706P2PID3
: TELEPHONE: 415/225-5530
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 352 amino acids

```

TYPE: Amino Acid
TOPOLOGY: Linear
US-08-801-228-4

Query Match 100.0%; Score 1830; DB 12; Length 352;
Best Local Similarity 100.0%; Pred. No. 2,1e-167;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MEGISITSDNYTEEMSGDYDSMKPCPFRENNANFNKIFLPTIYSIIFLTGIVGNGLVI 60
    |||||||
DB 1 MEGISITSDNYTEEMSGDYDSMKPCPFRENNANFNKIFLPTIYSIIFLTGIVGNGLVI 60
    |||||||
QY 61 LVMGYQKLLSMMDKYRLHLSVADLLFVITLPPFAVADVAVANWYFGNPLCAVAVHYIYVNL 120
    |||||||
DB 61 LVMGYQKLLSMMDKYRLHLSVADLLFVITLPPFAVADVAVANWYFGNPLCAVAVHYIYVNL 120
    |||||||
QY 121 YSSVLLIAFTSLDRYLAIIVATNSQRPRLAEKVVYVGVWIPALLTIPDFIFANVSEA 180
    |||||||
DB 121 YSSVLLIAFTSLDRYLAIIVATNSQRPRLAEKVVYVGVWIPALLTIPDFIFANVSEA 180
    |||||||
QY 181 DDRYICDRFPNDLMVVVFOQIIMVGLLPGIYILSCYCIISKLSHSGHOKRKALKT 240
    |||||||
DB 181 DDRYICDRFPNDLMVVVFOQIIMVGLLPGIYILSCYCIISKLSHSGHOKRKALKT 240
    |||||||
QY 241 TVIIILAFACWLPYYIGISIDSFILLEIIKGCEFEFNTVHKWISTEALAFHCCLNPI 300
    |||||||
DB 241 TVIIILAFACWLPYYIGISIDSFILLEIIKGCEFEFNTVHKWISTEALAFHCCLNPI 300
    |||||||
QY 301 LVAFLLGAKFKFTSAQHALTYSRGSLSKILSKGRGSHSVSTESSESSFHSS 352
    |||||||
DB 301 LVAFLLGAKFKFTSAQHALTYSRGSLSKILSKGRGSHSVSTESSESSFHSS 352
    |||||||

```

RESULT 5
US-08-801-238-4

```

: Sequence 4, Application US/08801238
: GENERAL INFORMATION:
: APPLICANT: Lee, James
: TITLE OF INVENTION: PFA4 RECEPTOR
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Winpatin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/801,238
: FILING DATE: 19-Feb-1997
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/284586
: FILING DATE: 10-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/076093
: FILING DATE: 11-JUN-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/810782
: FILING DATE: 19-DEC-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: P0706P2PID1
: TELEPHONE: 415/225-5530

```

TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-801-238-4

Query Match 100.0%; Score 1830; DB 12; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.1e-167;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGISITSDNYTEEMSGDYDSKMEPCFRENNANFNKIFLPTIYSIFLGIYNGLYI 60
 DB 1 MEGISITSDNYTEEMSGDYDSKMEPCFRENNANFNKIFLPTIYSIFLGIYNGLYI 60
 61 LVMGYQKKLRSMYDKYRLHLSVADLLFVITLPEVAVDVANWYFGNPLCKAVHYITVNL 120
 61 LVMGYQKKLRSMYDKYRLHLSVADLLFVITLPEVAVDVANWYFGNPLCKAVHYITVNL 120
 QY 121 YSSVLLIAFLSLDRYLAVHATNSQRPRLAEKVYVGVWIPALLTIPTIFANVSEA 180
 DB 121 YSSVLLIAFLSLDRYLAVHATNSQRPRLAEKVYVGVWIPALLTIPTIFANVSEA 180
 QY 181 DDRYICDRFYNDLMVYVFOQHIMVGLIPGIYILSCYCIISKLSHSGHOKRKALKT 240
 DB 181 DDRYICDRFYNDLMVYVFOQHIMVGLIPGIYILSCYCIISKLSHSGHOKRKALKT 240
 QY 241 TVILIAFFACWLPYYIGISIDSFILLEIKOGCEFEYVHKWISITBALAFFHCCLNPI 300
 DB 241 TVILIAFFACWLPYYIGISIDSFILLEIKOGCEFEYVHKWISITBALAFFHCCLNPI 300
 QY 301 LYAFLGAKFKTSAQHALLTVSRGSSLKILSKGRGHSSVSTESSSPHSS 352
 DB 301 LYAFLGAKFKTSAQHALLTVSRGSSLKILSKGRGHSSVSTESSSPHSS 352

RESULT 6

US-08-802-627-4

Sequence 4, Application US/08802627

GENERAL INFORMATION:

APPLICANT: Lee, James

TITLE OF INVENTION: NUCLEIC ACID ENCODING PFAA RECEPTOR

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Gentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Gentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/802.627

FILING DATE: 19-Feb-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/284586

FILING DATE: 10-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/076093

FILING DATE: 11-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/810782

FILING DATE: 19-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.
 REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: P07062P2ID2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-5530
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-802-627-4

Query Match 100.0%; Score 1830; DB 12; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.1e-167;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGISITSDNYTEEMSGDYDSKMEPCFRENNANFNKIFLPTIYSIFLGIYNGLYI 60
 DB 1 MEGISITSDNYTEEMSGDYDSKMEPCFRENNANFNKIFLPTIYSIFLGIYNGLYI 60
 61 LVMGYQKKLRSMYDKYRLHLSVADLLFVITLPEVAVDVANWYFGNPLCKAVHYITVNL 120
 61 LVMGYQKKLRSMYDKYRLHLSVADLLFVITLPEVAVDVANWYFGNPLCKAVHYITVNL 120
 QY 121 YSSVLLIAFLSLDRYLAVHATNSQRPRLAEKVYVGVWIPALLTIPTIFANVSEA 180
 DB 121 YSSVLLIAFLSLDRYLAVHATNSQRPRLAEKVYVGVWIPALLTIPTIFANVSEA 180
 QY 181 DDRYICDRFYNDLMVYVFOQHIMVGLIPGIYILSCYCIISKLSHSGHOKRKALKT 240
 DB 181 DDRYICDRFYNDLMVYVFOQHIMVGLIPGIYILSCYCIISKLSHSGHOKRKALKT 240
 QY 241 TVILIAFFACWLPYYIGISIDSFILLEIKOGCEFEYVHKWISITBALAFFHCCLNPI 300
 DB 241 TVILIAFFACWLPYYIGISIDSFILLEIKOGCEFEYVHKWISITBALAFFHCCLNPI 300
 QY 301 LYAFLGAKFKTSAQHALLTVSRGSSLKILSKGRGHSSVSTESSSPHSS 352
 DB 301 LYAFLGAKFKTSAQHALLTVSRGSSLKILSKGRGHSSVSTESSSPHSS 352

RESULT 7

US-08-802-627A-4

Sequence 4, Application US/08802627A

GENERAL INFORMATION:

APPLICANT: Lee, James

TITLE OF INVENTION: NUCLEIC ACID ENCODING PFAA RECEPTOR

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Gentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Gentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/802.627A

FILING DATE: 19-Feb-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/284586

FILING DATE: 10-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/076093

FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2P1D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-802-627A-4

Query Match 100.0%; Score 1830; DB 12; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.1e-167;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGISITSDNRYTEEMSGDYSKKEPCFRENNANFNKIFLPTIYSITFLTGIVNGLVI 60
DB 1 MEGISITSDNRYTEEMSGDYSKKEPCFRENNANFNKIFLPTIYSITFLTGIVNGLVI 60
QY 61 LVMGYOKKLSMTDKYRLHLSVADLLEFVITLPEWADVAVANMFGNFKCAVHYITYVNL 120
DB 61 LVMGYOKKLSMTDKYRLHLSVADLLEFVITLPEWADVAVANMFGNFKCAVHYITYVNL 120
QY 121 YSSVLLIAFLSLDRYLAIIVAHATNSQRPKLLAEKVVYVGVWIPALLTIPDFIFANVSEA 180
DB 121 YSSVLLIAFLSLDRYLAIIVAHATNSQRPKLLAEKVVYVGVWIPALLTIPDFIFANVSEA 180
QY 181 DDRIYICDRFYNDLWVYVFOFOHIMVGLIPGIYILSCYCIILSKLSHSGHQRKALKT 240
DB 181 DDRIYICDRFYNDLWVYVFOFOHIMVGLIPGIYILSCYCIILSKLSHSGHQRKALKT 240
QY 241 TVILILAFACWLPYIYIGISIDSFILLEIKQCEFEFNTVHKMISTEALAFHCCCLNPI 300
DB 241 TVILILAFACWLPYIYIGISIDSFILLEIKQCEFEFNTVHKMISTEALAFHCCCLNPI 300
QY 301 LYAFLGAKFTSAQHATLSVRSGLKILSKRGHSHSVSTESSESSFHSS 352
DB 301 LYAFLGAKFTSAQHATLSVRSGLKILSKRGHSHSVSTESSESSFHSS 352

RESULT 8
US-09-104-063-4
Sequence 4, Application US/09104063
GENERAL INFORMATION:
APPLICANT: Lee, James
APPLICANT: Wood, William I.
TITLE OF INVENTION: PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,063
FILING DATE: 24-June-1998
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/701265
FILING DATE: 22-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/664228
FILING DATE: 06-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-104-063-4

Query Match 100.0%; Score 1830; DB 15; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.1e-167;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGISITSDNRYTEEMSGDYSKKEPCFRENNANFNKIFLPTIYSITFLTGIVNGLVI 60
DB 1 MEGISITSDNRYTEEMSGDYSKKEPCFRENNANFNKIFLPTIYSITFLTGIVNGLVI 60
QY 61 LVMGYOKKLSMTDKYRLHLSVADLLEFVITLPEWADVAVANMFGNFKCAVHYITYVNL 120
DB 61 LVMGYOKKLSMTDKYRLHLSVADLLEFVITLPEWADVAVANMFGNFKCAVHYITYVNL 120
QY 121 YSSVLLIAFLSLDRYLAIIVAHATNSQRPKLLAEKVVYVGVWIPALLTIPDFIFANVSEA 180
DB 121 YSSVLLIAFLSLDRYLAIIVAHATNSQRPKLLAEKVVYVGVWIPALLTIPDFIFANVSEA 180
QY 181 DDRIYICDRFYNDLWVYVFOFOHIMVGLIPGIYILSCYCIILSKLSHSGHQRKALKT 240
DB 181 DDRIYICDRFYNDLWVYVFOFOHIMVGLIPGIYILSCYCIILSKLSHSGHQRKALKT 240
QY 241 TVILILAFACWLPYIYIGISIDSFILLEIKQCEFEFNTVHKMISTEALAFHCCCLNPI 300
DB 241 TVILILAFACWLPYIYIGISIDSFILLEIKQCEFEFNTVHKMISTEALAFHCCCLNPI 300
QY 301 LYAFLGAKFTSAQHATLSVRSGLKILSKRGHSHSVSTESSESSFHSS 352
DB 301 LYAFLGAKFTSAQHATLSVRSGLKILSKRGHSHSVSTESSESSFHSS 352

RESULT 9
US-09-104-296-4
Sequence 4, Application US/09104296
GENERAL INFORMATION:
APPLICANT: Lee, James
APPLICANT: Wood, William I.
TITLE OF INVENTION: PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

RESULT 10
US-09-122-068-2
Sequence 2, Application US/09122068
GENERAL INFORMATION:
APPLICANT: PILARSENTHI, KODANDARAM
APPLICANT: GUPTA, SHALLEE
TITLE OF INVENTION: CXCR4B: A HUMAN SPICE VARIANT
TITLE OF INVENTION: CXCR4 CHEMOKINE RECEPTOR

RESULT 11
US-08-182-962-6
; Sequence 6, Application US/08182962
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun

```

1  TITLE OF INVENTION:  PROTEIN RECEPTORS
2  NUMBER OF SEQUENCES:  14
3  CORRESPONDENCE ADDRESS:
4  ADDRESSEE:  Cooley Godward Castro Huddleson & Tatum
5  STREET:  5 Palo Alto Square
6  CITY:  Palo Alto
7  STATE:  California
8  COUNTRY:  USA
9  ZIP:  94306-2155
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE:  Floppy disk
12 COMPUTER:  IBM PC compatible
13 OPERATING SYSTEM:  PC-DOS/MS-DOS
14 SOFTWARE:  PatentIn Release #1.0, Version #1.25
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER:  US/08/446,669
17 FILING DATE:  May 25, 1995
18 CLASSIFICATION:  435
19 ATTORNEY/AGENT INFORMATION:
20 NAME:  Neeley, Richard
21 REGISTRATION NUMBER:  30,092
22 REFERENCE/DOCKET NUMBER:  UCAL-237/01US
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE:  415-845-5000
25 TELEFAX:  415-857-0663
26 TELEX:  380816CCOOLEYPA
27 INFORMATION FOR SEQ ID NO:  6:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH:  352 amino acids
30 TYPE:  amino acid
31 TOPOLOGY:  linear
32 MOLECULE TYPE:  protein
33 HYPOTHETICAL:  NO
34 US-08-446-669-6

```

Query Match	97.88;	Score 1789;	DB 7;	Length 352;
Best Local Similarity	98.38;	Pred. No. 1.8e-163;		
Matches 346;	Conservative	0;	Mismatches 6;	Indels 0;
				Gaps 0;

QY	1	MEGSIATSDNYTEMSGSDJDSKKECFEENANFNKILPTIYSITFTGIVGNLVI	60
Db	1	MEGSIATSDNYTEMSGSDJDSKKECFEENANFNKILPTIYSITFTGIVGNLVI	60
QY	61	LYMGQKKLSMTDKYRLHLVSADLFTVLPEMAVDVANWYFQNLCKAVHYITVNL	120
Db	61	LYMGQKKLSMTDKYRLHLVSADLFTVLPEMAVDVANWYFQNLCKAVHYITVNL	120
QY	121	YSSVLLIAFLSDBYLIAVHAATNSQBRKLLAEVYVVGWVIPAALLIIPDFIFANSEA	180
Db	121	YSSVLLIAFLSDBYLIAVHAATNSQBRKLLAEVYVVGWVIPAALLIIPDFIFANSEA	180
QY	181	DDRYICDRFYNDLAMYVVOFOHIMWBLIPGIYILSCYCIITLSKLSHGOKRKALKT	240
Db	181	DDRYICDRFYNDLAMYVVOFOHIMWBLIPGIYILSCYCIITLSKLSHGOKRKALKT	240
QY	241	TVILILAFACMLPYUYGISIDSFILLEIIKQGCPEFNTVHKMISTEALAFHCCCLNPI	300
Db	241	TVILILAFACMLPYUYGISIDSFILLEIIKQGCPEFNTVHKMISTEALAFHCCCLNPI	300
QY	301	LYALFLAKFTISAQHALTVSRGSLKILSKRGKGHSVSTSESSSFHSS 352	
Db	301	LYALFLAKFTISAQHALTVSRGSLKILSKRGKGHSVSTSESSSFHSS 352	

RESULT 13
US-08-450-393-6
Sequence 6, Application US/08450393
GENERAL INFORMATION:
INVENTOR: CHANG, CHIAO-CHANG
APPLICANT: Charo, Israel
TITLE OF INVENTION: MAMMALIAN MONOCYTE
PROTEIN RECEPTORS
TITLE OF INVENTION: MAMMALIAN MONOCYTE
CHEMOKINE RECEPTORS

NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooley Goddard Castro Huddleson & Tatum
 STREET: 5 Palo Alto Square
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94306-2155
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/450,393
 FILING DATE: May 25, 1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Cseert, Luanan
 REGISTRATION NUMBER: 31,822
 REFERENCE/DOCKET NUMBER: UCAL-237/020US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-843-5165
 TELEFAX: 415-8857-0663
 TELEX: 380816COOLEYPA
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: NO
 US-08-450-393-6

Query Match 97.8%; Score 1789; DB 7; Length 352;
 Best Local Similarity 98.3%; Pred. No. 1.8e-163;
 Matches 346; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY	1	MEGIITYSDNYTEMGSGDYDMSKPECFREANFNKIFLPTIYSIIFLTGIVNGGLVI	60
DB	1	MESITTYSDNTTEMGSGDYDMSKPECFREANFNKIFLPTIYSIIFLTGIVNGGLVI	60
QY	61	LVMGYQKLRSTDKYRLHLVADLLFVITLPEFMAVDAAVMYFGNFKCAVHYITVNL	120
DB	61	LVMGYQKLRSTDKYRLHLVADLLFVITLPEFMAVDAAVMYFGNFKCAVHYITVNL	120
QY	121	YSSVLIAFISLDRIALVHATNSQRPRLAEKVYVGVWIPALLITPDIIFANVSEA	180
DB	121	YSSVLIAFISLDRIALVHATNSQRPRLAEKVYVGVWIPALLITPDIIFANVSEA	180
QY	181	DDRYICDREYPNDLVVVFQFHIMVGLIPGIVILSCYCIITISKLSHGKQRKALMT	240
DB	181	DDRYICDREYPNDLVVVFQFHIMVGLIPGIVILSCYCIITISKLSHGKQRKALMT	240
QY	241	TYVILLIAFACWLPYYIGISIDSIFLLEITIKQCEFEENTVHKWISTEALAFHCLNPI	300
DB	241	TYVILLIAFACWLPYYIGISIDSIFLLEITIKQCEFEENTVHKWISTEALAFHCLNPI	300
QY	301	LVAFGLAKFKTSQAQHALTSVSRGSSILKSKRGKGGHSSVTESESSSFHSS	352
DB	301	LVAFGLAKFKTSQAQHALTSVSRGSSILKSKRGKGGHSSVTESESSSFHSS	352

RESULT 14
 US-07-977-452A-21
 Sequence 21, Application US/07977452A
 GENERAL INFORMATION:
 APPLICANT: Godiska, Ronald
 APPLICANT: Gray, Patrick W.
 APPLICANT: Schweiakart, Vicki L.
 TITLE OF INVENTION: Novel Seven Transmembrane Receptors
 NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ADDRESSEE: Bicknell
 STREET: Two First National Plaza, Suite 2100
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60603
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/977,452A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Noland, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 30928
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 346-5750
 TELEFAX: (312) 984-9740
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 337 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-977-452A-21

Query Match 95.7%; Score 1752; DB 2; Length 337;
 Best Local Similarity 100.0%; Pred. No. 5.9e-160;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	16	MGSGDYDMSKPECFREANFNKIFLPTIYSIIFLTGIVNGGLVIYMGYQKLRSTDK	75
DB	1	MESGDIYDMSKPECFREANFNKIFLPTIYSIIFLTGIVNGGLVIYMGYQKLRSTDK	60
QY	76	YRLHLVADLLFVITLPEFMAVDAAVMYFGNFKCAVHYITVNLVSSVLIATISDRY	135
DB	61	YRLHLVADLLFVITLPEFMAVDAAVMYFGNFKCAVHYITVNLVSSVLIATISDRY	120
QY	136	LAIYHATNSQRPRLAEKVYVGVWIPALLITPDIIFANVSEADRYICDREYPNDLV	195
DB	121	LAIYHATNSQRPRLAEKVYVGVWIPALLITPDIIFANVSEADRYICDREYPNDLV	180
QY	196	VVVFQFHIMVGLIPGIVILSCYCIITISKLSHGKQRKALMTVYVILLIAFACWLPY	255
DB	181	VVVFQFHIMVGLIPGIVILSCYCIITISKLSHGKQRKALMTVYVILLIAFACWLPY	240
QY	256	YIGISIDSIFLLEITIKQCEFEENTVHKWISTEALAFHCLNPIYVAFGLAKFKTSQ	315
DB	241	YIGISIDSIFLLEITIKQCEFEENTVHKWISTEALAFHCLNPIYVAFGLAKFKTSQ	300
QY	316	ALTSVSRGSSILKSKRGKGGHSSVTESESSSFHSS	352
DB	301	ALTSVSRGSSILKSKRGKGGHSSVTESESSSFHSS	337

RESULT 15
 US-08-245-242-46
 Sequence 46, Application US/08245242
 GENERAL INFORMATION:
 APPLICANT: Godiska, Ronald
 APPLICANT: Gray, Patrick W.
 APPLICANT: Schweiakart, Vicki L.
 TITLE OF INVENTION: Novel Seven Transmembrane Receptors
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 14, 1999, 09:50:15 : Search time 10.08 Seconds

(without alignments)
344.610 Million cell updates/sec

Title: US-09-104-063-4

Perfect score: 1830

Sequence: 1 MEGISITSDNYTEEMSGSD.....KRGHSSVSTRESSSPHSS 352

Scoring table: BLOSUM62

Searched: 106577 seqs, 9868381 residues

Database : Issued Patents-AA:*

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/PCTUS9.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1830	100.0	352	1	US-08-202-056-3	Sequence 3, Appl1
2	1830	100.0	352	1	US-08-076-093A-4	Sequence 4, Appl1
3	1830	100.0	352	2	US-08-701-265-4	Sequence 4, Appl1
4	1830	100.0	352	2	US-08-284-586-4	Sequence 4, Appl1
5	1830	100.0	352	2	US-08-805-478-4	Sequence 4, Appl1
6	1789	97.8	352	1	US-08-450-393A-6	Sequence 6, Appl1
7	1789	97.8	352	3	PCT-US95-00476-6	Sequence 6, Appl1
8	1752	95.7	337	2	US-08-153-848-46	Sequence 6, Appl1
9	1752	95.7	337	3	PCT-US93-11153-46	Sequence 46, Appl1
10	568	31.0	355	1	US-07-759-568-1	Sequence 1, Appl1
11	568	31.0	355	1	US-08-202-056-7	Sequence 1, Appl1
12	568	31.0	355	1	US-08-450-393A-8	Sequence 8, Appl1
13	568	31.0	355	3	PCT-US95-00476-8	Sequence 8, Appl1
14	557.5	30.5	350	1	US-08-202-056-1	Sequence 1, Appl1
15	557.5	30.5	350	1	US-08-076-093A-2	Sequence 2, Appl1
16	557.5	30.5	350	1	US-08-450-393A-7	Sequence 7, Appl1
17	557.5	30.5	350	2	US-08-410-453A-1	Sequence 1, Appl1
18	557.5	30.5	350	2	US-08-701-265-2	Sequence 2, Appl1
19	557.5	30.5	350	2	US-08-410-454A-1	Sequence 1, Appl1
20	557.5	30.5	350	2	US-08-284-586-2	Sequence 2, Appl1
21	557.5	30.5	350	2	US-08-410-456A-1	Sequence 1, Appl1
22	557.5	30.5	350	2	US-08-805-478-2	Sequence 2, Appl1
23	557.5	30.5	350	2	PCT-US95-00476-7	Sequence 7, Appl1
24	557.5	30.4	378	2	US-08-153-848-7	Sequence 7, Appl1
25	557.5	30.4	378	2	US-08-153-848-15	Sequence 15, Appl1
26	557.5	30.4	378	2	US-08-153-848-19	Sequence 19, Appl1
27	557.5	30.4	410	3	PCT-US93-11153-7	Sequence 7, Appl1
28	557.5	30.4	378	3	PCT-US93-11153-15	Sequence 15, Appl1
29	557.5	30.4	359	2	PCT-US93-11153-19	Sequence 19, Appl1
30	550	30.1	359	2	US-08-153-848-24	Sequence 24, Appl1
31	550	30.1	359	2	PCT-US93-11153-24	Sequence 24, Appl1
32	549.5	30.0	355	2	US-08-153-848-28	Sequence 28, Appl1
33	549.5	30.0	355	2	US-08-153-848-32	Sequence 32, Appl1
34	549.5	30.0	355	3	PCT-US93-11153-32	Sequence 32, Appl1
35	549.5	30.0	355	3	PCT-US93-11153-32	Sequence 32, Appl1
36	540	29.5	372	1	US-08-202-056-5	Sequence 5, Appl1
37	540	29.5	372	1	US-08-076-093A-6	Sequence 6, Appl1
38	540	29.5	372	1	US-08-701-265-6	Sequence 6, Appl1
39	540	29.5	372	2	US-08-284-586-6	Sequence 6, Appl1

40	540	29.5	372	2	US-08-805-478-6	Sequence 6, Appl1
41	538	29.4	378	1	US-08-383-750-2	Sequence 2, Appl1
42	538	29.4	378	2	US-08-383-751A-2	Sequence 2, Appl1
43	538	29.4	378	3	PCT-US93-09636-2	Sequence 2, Appl1
44	528	28.9	374	1	US-08-450-393A-2	Sequence 2, Appl1
45	528	28.9	374	3	PCT-US95-00476-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-202-056-3
Sequence 3, Application US/08202056

Patent No. 5440021

GENERAL INFORMATION:

APPLICANT: Chuntcharapai, Anan

APPLICANT: Hebert, Caroline

APPLICANT: Kim, Kyung Jin

APPLICANT: Lee, James

TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/202,056

FILING DATE: 25-FEB-1994

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/677211

FILING DATE: 29-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: 706P3

TELEPHONE: 415/225-5530

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-202-056-3

Query Match 100.0%; Score 1830; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6,4e-144;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEGISITSDNYTEEMSGDYDSKPECPFEENANFKIFLPTYSITFTGIYGNGLVI	60
DB	1	MEGISITSDNYTEEMSGDYDSKPECFEENANFKIFLPTYSITFTGIYGNGLVI	60
QY	61	LVMGYQKRLSMYDKYRLHLSVADLFTVTLPEWAVDAVAMVFGNFLCAVHYITVNL	120
DB	61	LVMGYQKRLSMYDKYRLHLSVADLFTVTLPEWAVDAVAMVFGNFLCAVHYITVNL	120
QY	121	YSSVLLIAFLISLDYRLAIVATNSORPRKLLAEVYVGVWIPALLITPDFTFANVSEA	180
DB	121	YSSVLLIAFLISLDYRLAIVATNSORPRKLLAEVYVGVWIPALLITPDFTFANVSEA	180

TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-805-478-4

Query Match 100.0%; Score 1830; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.4e-144;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGISITSDNTYEMSGSDYDSMKPCFRENANFNKIFLPTIYSIFLITGVNGLYI 60
DB 1 MEGISITSDNTYEMSGSDYDSMKPCFRENANFNKIFLPTIYSIFLITGVNGLYI 60
QY 61 LVNGYOKRLSMTDKYRLHLVADLLEFVITLPEWAVDAVANNYFGNPLCKAVHYITVNL 120
DB 61 LVNGYOKRLSMTDKYRLHLVADLLEFVITLPEWAVDAVANNYFGNPLCKAVHYITVNL 120
QY 121 YSSVLLIAFISLDRLAIVATNSQRPRLAEKVYVGVWIPALLITPDIIFANVSEA 180
DB 121 YSSVLLIAFISLDRLAIVATNSQRPRLAEKVYVGVWIPALLITPDIIFANVSEA 180
QY 181 DDRICDREFPNLMVWVFOFOHIMVGLIPGIVILSCYCIISKLSHSGHQKRAKLT 240
DB 181 DDRICDREFPNLMVWVFOFOHIMVGLIPGIVILSCYCIISKLSHSGHQKRAKLT 240
QY 241 TVILILAFACWLPYYIGISIDSFILLETIKGCEPENTVHKWISTEALAFHCCLNPI 300
DB 241 TVILILAFACWLPYYIGISIDSFILLETIKGCEPENTVHKWISTEALAFHCCLNPI 300
QY 301 LVAFLEAKFTSAQHATLSVSRGSSILKLSKGRGSHSVSTESSESSPHSS 352
DB 301 LVAFLEAKFTSAQHATLSVSRGSSILKLSKGRGSHSVSTESSESSPHSS 352

RESULT 6
US-08-450-393A-6
Sequence 6, Application US/08450393A
Patent No. 5707815

GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cseert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/020US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEFAX: 415-8857-0663

TELEX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-450-393A-6

Query Match 97.8%; Score 1789; DB 1; Length 352;
Best Local Similarity 98.3%; Pred. No. 1.5e-140;
Matches 346; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MEGISITSDNTYEMSGSDYDSMKPCFRENANFNKIFLPTIYSIFLITGVNGLYI 60
DB 1 MEGISITSDNTYEMSGSDYDSMKPCFRENANFNKIFLPTIYSIFLITGVNGLYI 60
QY 61 LVNGYOKRLSMTDKYRLHLVADLLEFVITLPEWAVDAVANNYFGNPLCKAVHYITVNL 120
DB 61 LVNGYOKRLSMTDKYRLHLVADLLEFVITLPEWAVDAVANNYFGNPLCKAVHYITVNL 120
QY 121 YSSVLLIAFISLDRLAIVATNSQRPRLAEKVYVGVWIPALLITPDIIFANVSEA 180
DB 121 YSSVLLIAFISLDRLAIVATNSQRPRLAEKVYVGVWIPALLITPDIIFANVSEA 180
QY 181 DDRICDREFPNLMVWVFOFOHIMVGLIPGIVILSCYCIISKLSHSGHQKRAKLT 240
DB 181 DDRICDREFPNLMVWVFOFOHIMVGLIPGIVILSCYCIISKLSHSGHQKRAKLT 240
QY 241 TVILILAFACWLPYYIGISIDSFILLETIKGCEPENTVHKWISTEALAFHCCLNPI 300
DB 241 TVILILAFACWLPYYIGISIDSFILLETIKGCEPENTVHKWISTEALAFHCCLNPI 300
QY 301 LVAFLEAKFTSAQHATLSVSRGSSILKLSKGRGSHSVSTESSESSPHSS 352
DB 301 LVAFLEAKFTSAQHATLSVSRGSSILKLSKGRGSHSVSTESSESSPHSS 352

RESULT 7
PCT-US95-00476-6
Sequence 6, Application PC/TUS9500476
GENERAL INFORMATION:

APPLICANT: The Regents of the University of California
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-291
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-977-1001
TELEFAX: 310-977-1003
TELEX:
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
PCT-US95-00476-6

Query Match 97.8%; Score 1789; DB 3; Length 352;
Best Local Similarity 98.3%; Pred. No. 1.5e-140;
Matches 346; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MEGSITSDNYTEEMSGDYDSKKEPCFREENANFNKIFLPTIYSIFLTGIVGNGLYI 60
DB 1 MEGSITSDNYTEEMSGDYDSKKEPCFREENANFNKIFLPTIYSIFLTGIVGNGLYI 60
QY 61 LVMGYQKRLSMYTDKRYLHLSVADLLEVTLPFWAVDAVANMYFGNFCRAVHYIYTVNL 120
DB 61 LVMGYQKRLSMYTDKRYLHLSVADLLEVTLPFWAVDAVANMYFGNFCRAVHYIYTVNL 120
QY 121 YSSVLLIAFISLDRIYLAIVHATNSQRPRLAEKVYVGVWIPALLTTPDFIFANVSEA 180
DB 121 YSSVLLIAFISLDRIYLAIVHATNSQRPRLAEKVYVGVWIPALLTTPDFIFANVSEA 180
QY 181 DDIRICDRFPNDLMVVFQFOHIMVGLIPGIVILSCYCIISKLSHSGHQRKALKT 240
DB 181 DDIRICDRFPNDLMVVFQFOHIMVGLIPGIVILSCYCIISKLSHSGHQRKALKT 240
QY 241 TVLLIAFACMLPYIYIGISIDSFILLEIIRKQCEFEFNTVHKWISTEALAFHCCLNPI 300
DB 241 TVLLIAFACMLPYIYIGISIDSFILLEIIRKQCEFEFNTVHKWISTEALAFHCCLNPI 300
QY 301 LYALGAKFKTSAQHATLSVSRGSSLKILSKGRGHSVSTESSESSFHSS 352
DB 301 LYALGAKFKTSAQHATLSVSRGSSLKILSKGRGHSVSTESSESSFHSS 352

RESULT 8
US-08-153-848-46

Sequence 46, Application US/08153848
Patent No. 5759804
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwellkart, Vicki L.
TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-848-46

Query Match 95.7%; Score 1752; DB 2; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.6e-137;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MGSQDYDSMKKEPCFREENANFNKIFLPTIYSIFLTGIVGNGLYLVMGYQKRLRSMYTDK 75
DB 1 MGSQDYDSMKKEPCFREENANFNKIFLPTIYSIFLTGIVGNGLYLVMGYQKRLRSMYTDK 75
QY 76 YRLHLSVADLLEVTLPFWAVDAVANMYFGNFCRAVHYIYTVNLSSVLLIAFISLDRIY 135
DB 61 YRLHLSVADLLEVTLPFWAVDAVANMYFGNFCRAVHYIYTVNLSSVLLIAFISLDRIY 120
QY 136 LAIVHATNSQRPRLAEKVYVGVWIPALLTTPDFIFANVSADDRYICDRFPNDLM 195
DB 121 LAIVHATNSQRPRLAEKVYVGVWIPALLTTPDFIFANVSADDRYICDRFPNDLM 180
QY 196 VVVFQFOHIMVGLIPGIVILSCYCIISKLSHSGHQRKALKTVYLLIAFAFCMLPY 255
DB 181 VVVFQFOHIMVGLIPGIVILSCYCIISKLSHSGHQRKALKTVYLLIAFAFCMLPY 240
QY 256 YIGISIDSFILLEIIRKQCEFEFNTVHKWISTEALAFHCCLNPIYALGAKFKTSAQH 315
DB 241 YIGISIDSFILLEIIRKQCEFEFNTVHKWISTEALAFHCCLNPIYALGAKFKTSAQH 300
QY 316 ALTSVSRGSSLKILSKGRGHSVSTESSESSFHSS 352
DB 301 ALTSVSRGSSLKILSKGRGHSVSTESSESSFHSS 337

RESULT 9

PCT-US93-11153-46
Sequence 46, Application PC/TUS9311153
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwellkart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-11153-46

Query Match 95.7%; Score 1752; DB 3; Length 337;
Best Local Similarity 100.0%; Pred. No. 1,6e-137; Mismatches 0; Indels 0; Gaps 0;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MCGSDYDKKEPCFRENNANENKIFLPTIYSIIIFLTGIVNGVLIVMGYQKRLSMTDK 75
DB 1 MCGSDYDKKEPCFRENNANENKIFLPTIYSIIIFLTGIVNGVLIVMGYQKRLSMTDK 60
QY 76 YRLHLSVADLLFVITLPPMAVDVANWYFGNFLCAVHYITVNVXSVLLIAFTSLDRY 135
DB 61 YRLHLSVADLLFVITLPPMAVDVANWYFGNFLCAVHYITVNVXSVLLIAFTSLDRY 120
QY 136 LAIVHATISORPRKLLAEKVYVGVWIPALLTIPDEFIFANVSEADDRICDRFPNDLM 195
DB 121 LAIVHATISORPRKLLAEKVYVGVWIPALLTIPDEFIFANVSEADDRICDRFPNDLM 180
QY 196 VVVFQFQHMVGLIPGIVILSCYCIISKLSHSGHOKRKALKTTVILLIAFACWLPY 255
DB 181 VVVFQFQHMVGLIPGIVILSCYCIISKLSHSGHOKRKALKTTVILLIAFACWLPY 240
QY 256 YIGISIDFILLEITKOCCEPENTVHKMISTITREALAFHCCNPLTLYAFIAKKEFTSQH 315
DB 241 YIGISIDFILLEITKOCCEPENTVHKMISTITREALAFHCCNPLTLYAFIAKKEFTSQH 300
QY 316 ALTSVRSGLSKILSKGRGHSVSTSESSSFHSS 352
DB 301 ALTSVRSGLSKILSKGRGHSVSTSESSSFHSS 337

RESULT 10
US-07-759-568-1
Sequence 1, Application US/07759568
Patent No. 5374506
GENERAL INFORMATION:
APPLICANT: Murphy, Philip M.
TITLE OF INVENTION: Cloning of cDNA Encoding a Functional
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cushman, Darby & Cushman
STREET: 1615 L Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/759, 568
FILING DATE: 19910913
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Scott, Watson T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: WTS/5683/91535/WBH
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 cush
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-759-568-1

Query Match 31.0%; Score 568; DB 1; Length 355;
Best Local Similarity 35.3%; Pred. No. 6,7e-40; Mismatches 119; Indels 54; Gaps 11;
Matches 132; Conservative 69; Mismatches 119; Indels 54; Gaps 11;

QY 9 SDNYT-----EMSGSDYSM-----KEPCFRENNANENKIFLPTIYSIIIFLTGIVN 56
DB 3 SDSFEDFMKGBDLSNYSYSTLPFLDPAAC-EPESLEINKYFVITLYALVFLSLGN 61
QY 57 GLVIVMGYQKRLSMTDKYRLHLSVADLLFVITLPPMAVDVANWYFGNFLCAVHYIY 116
DB 62 SLVMLVILYSVGRSVTDVYLLNLADLPALTLPMAASKVGVWIFGTFELCVSILK 121
QY 117 TVNLYSVLLIAFTSLDRYLAIVHATISORPRKLLAEKVYVGVWIPALLTIPDEFI-- 175
DB 122 EVNPFSGILLACISVDKYLIVHATITLTKRLV-KFICLSIWGSLALAVLLFRR 180
QY 175 ---ANVSEADDRICDRFPNDL--VVVFQFQHMVGLIPGIVILSCYCIISKLSH 228
DB 181 TVYSSNVSPA-----CYEDMGNTANWRLRLIPQSFGEIVPLIMLFCVGLTRLEK 235
QY 229 SKGOKRKALKTYVILLIAFACWLPYIGISIDFILLEITKOCCEPENTVHKMISTITE 288
DB 236 AHMGCKHAKMVIYAVVILFLCWPYNLVLAJTLMTQVIOETCERRNIDALDATE 295
QY 289 ALAFHCCNPLIYAFIAKKEFTSAOHALTSVRSGLSKILSKGRGHSVSTES--- 345
DB 296 ILGILHSCNPLIYAFIAKKEFTSAOHALTSVRSGLSKILSKGRGHSVSTES--- 345
QY 345 -----ESSSFHSS 352
DB 339 SRPSFVGSSSGHTS 352

RESULT 11
US-08-202-056-7
Sequence 7, Application US/08202056
Patent No. 5440021
GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Hebert, Caroline
APPLICANT: Kim, Kyung Jin
APPLICANT: Lee, James
TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202, 056
FILING DATE: 25-FEB-1994
CLASSIFICATION: 436

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-291
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-977-1001
TELEFAX: 310-977-1003
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
PCT-US95-00476-8

Query Match 31.0%; Score 568; DB 3; Length 355;
Best Local Similarity 35.3%; Pred. No. 6,7e-40;
Matches 132; Conservative 69; Mismatches 119; Indels 54; Gaps 11;

QY 9 SDNYT-----EEMSGDYDSM-----KEPCFREMANFNKIFLPTIYSIIFLTGIYGN 56
DB 3 SDSFEDFWKGEDLSNYSYSTLPPLDAPC-EPESLEINKYFVYIYALVFLSLGN 61
QY 57 GIVILVMGYOKRLBSMTQKRYRLHLSVADLFFITLPEFNAVDAVAMVYGNFCKAVHYIY 116
DB 62 SLVMIYILSRGRSVTDVYLLNLADLLEFALTLPIYMAKSVNGWINGTFLCKVSLK 121
QY 117 TVNLSVYLIAFISLDRIYLAIVHATNSQRPRLAEKVVYGVWIPALLTIIPDFIF-- 175
DB 122 EVNEFSGLLLACISVDRLAIVHATRLITQKRYLV-KFICISINGLSLLALPVLPRR 180
QY 175 ----ANSEADDRYICDRFYPNDL--WVVFQOHIMVGLIPGIYILSCYCIISKLSH 228
DB 181 TVYSNVSPPA-----CYEDMGNNNTANMRLILPDSFGFIVPLIMLFCYGFLLTLEK 235
QY 229 SKGHOKRKALKTTVILLIAFFACWLPYIGISIDSFILLEIKOGCEFEFNTVHKMISTE 288
DB 236 AHMGQRHARMYIFAVLVLELCWLPYNLVLLADTLMRTQVIOETCERRNHIDRALDATE 295
QY 289 ALAFPHCLNPIYLAFLGAKFKTSQHALTSYRSGSLKILSKGRGSHSVSTES---- 345
DB 296 ILGIHLSCLNPIYLAFLGAKFKR-----HGL-----LKIILAI-----HGLISKSLPRD 338
QY 345 -----ESSFHS 352
DB 339 SRPFSVGSSTGHTS 352

RESULT 14
US-08-202-056-1
Sequence 1, Application US/08202056
Patent No. 5440021
GENERAL INFORMATION:
APPLICANT: Chuntharapal, Anan
APPLICANT: Hebert, Caroline
APPLICANT: Kim, Kyung Jin
APPLICANT: Lee, James
TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,056
FILING DATE: 25-FEB-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-202-056-1

Query Match 30.5%; Score 557.5; DB 1; Length 350;
Best Local Similarity 38.2%; Pred. No. 4.9e-39;
Matches 121; Conservative 56; Mismatches 127; Indels 13; Gaps 6;

QY 11 NYTEMGSGDYDSMKEPCFREMANFNKIFLPTIYSIIFLTGIYNGVILVMGYOKRLR 70
DB 16 NFT--GMPADEDEYSPCLM-ETETLNKYVVIYIYALVFLSLGNSLMLVILYSRGR 71
QY 71 SMTDKRYHLHSVADLFFITLPEFNAVDAVAMVYGNFCKAVHYIYTVNLYSSVILAFI 130
DB 72 SVTDVYLLNLADLLEFALTLPIYMAKSVNGWINGTFLCKVSLKLENEFSGLILACI 131
QY 131 SLDRIYLAIVHATNSQRPRLAEKVVYGVWIPALLTIIPDFIFANVSEADDRY-ICDRF 189
DB 132 SVDRILAVHATRLITQKRYLV-KFVCLGCGLSMNLSPFLPRQAHHPNNSPVCEY 190
QY 190 YPNDL--WVVFQOHIMVGLIPGIYILSCYCIISKLSHSGHOKRKALKTTVILILA 247
DB 191 LGNDTAKRMVYLRILPHTFGFIPLFVLMFCYGFLLRFLFAHMGQRHARMYIFAVVLI 250
QY 248 FFACWLPYIGISIDSFILLEIKOGCEFEFNTVHKMISTALAFPHCLNPIYLAFLGA 307
DB 251 FLLCWLPYNLVLLADTLMRTQVIOETCERRNIGRALTATEILGFLHCLNPIYLAFLGQ 310
QY 308 KF-----KTSQHALTS 319
DB 311 NFRHGFLKIILMHGLYS 327

RESULT 15
US-08-076-093A-2
Sequence 2, Application US/08076093A
Patent No. 5543503
GENERAL INFORMATION:
APPLICANT: Chuntharapal, Anan
APPLICANT: Hebert, Caroline
APPLICANT: Lee, James
APPLICANT: Jin Kim, K
TITLE OF INVENTION: Antibodies to Human PFA4 Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-076-093A-2

Query Match 30.5%; Score 557.5; DB 1; Length 350;
Best Local Similarity 38.2%; Pred. No. 4.9e-39;
Matches 121; Conservative 56; Mismatches 127; Indels 13; Gaps 6;

QY 11 NTEEMSGSDYDSMKPEPCREANANKIFLPITYSIIFLTGIVNGLVILVNGYOKLR 70
16 NPT--GMPRADEDSPCML-ETETLNKYVVIAYVALVFLSLGNSLVMLVILYSRVGR 71
QY 71 SMTDKYRLHSVADLLFVTLPPMAVDVAVANMYEGNLCRAVHYITVNLSSVLIAFI 130
72 SVTDVYLLNLADLLFALTLPIMASKVNGWTFGLCKVSLKEVNFSGILLACI 131
QY 131 SLDRYLAIVHATNSORPRKLAEKVVYVGMIPALLITPDIFANVSEADRY-ICDRF 189
132 SVDRYLAIVHATRTLTQKRHLV-KFVCLGQWLSMNLSPFLFQAAYHPNNSPCYEY 190
QY 190 YPNDL--WVVVFOFOHIMGLIPGIVILSCYIITSKLSHGOKRAKAKTTVILILA 247
191 LQNDYAKMWMVRLIPHTGFIIVPLFVMLCYGFTLRTLFKAMGOKHRAMRVIAFVVL 250
QY 248 FFACWLPYYIGISIDSFILLEIKQCEFEENTYHKWISITKALFPHCCINPLTYAFLGA 307
251 FLICWLPYVNLVLDLMTQVIGETCERRNNIGRALDATEIIGFLHSCINPLITYAFIGO 310
QY 308 KF----KTSQHAITS 319
311 NFRHGFLKILAMHGLVS 327
DB

Search completed: September 14, 1999, 09:51:01
Job time: 46 sec

Gencore version 4.5
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OM protein - protein search, using sw model

Run on: September 14, 1999, 09:50:15; Search time 14.3 Seconds

(without alignments)
583.043 Million cell updates/sec

Title: US-09-104-063-4

Perfect score: 1830

Sequence: 1 MEGISITYSDNTEEMSGSD.....KRGHSSVSTSESSSFHSS 352

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database: A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1830	100.0	352	1	Human monocytic P4
2	1830	100.0	352	1	Chemokine superfamily
3	1819	99.4	352	1	New platelet factor
4	1808	98.8	356	1	G-protein coupled
5	1752	95.7	337	1	Human RM3 seven tr
6	1742	95.2	337	1	Seven transmembran
7	1678.5	91.7	359	1	A murine CXCR2 chemo
8	597.5	32.7	360	1	Chemokine receptor
9	578	31.6	367	1	Rodent chemokine r
10	576.5	31.5	368	1	Human IP-10/Mig re
11	574	31.4	360	1	Recombinant high a
12	568.5	31.1	1064	1	IL8-R type 2-GBP 1
13	568	31.0	350	1	Sequence in a low
14	568	31.0	355	1	Human IL-8 recepto
15	568	31.0	360	1	Interleukin 8 rece
16	567.5	31.0	415	1	Human G-protein ch
17	564	30.8	355	1	Sequence in a high
18	564	30.8	355	1	Recombinant high a
19	560	30.6	378	1	Putative seven tra
20	559.5	30.6	350	1	Interleukin-8 rece
21	558	30.5	358	1	Recombinant high a
22	557.5	30.5	350	1	Interleukin-8 rece
23	557.5	30.5	1060	1	IL8-R type 1-GBP 1
24	557.5	30.5	350	1	Interleukin 8 rece
25	557.5	30.5	350	1	Recombinant high a
26	557	30.4	410	1	Putative seven tra
27	557	30.4	358	1	Partial sequence o
28	557	30.4	410	1	Polypeptide sequen
29	557	30.4	378	1	Human V31 seven tr
30	550	30.1	359	1	Seven transmembran
31	550	30.1	359	1	Murine V31 seven t
32	549.5	30.0	355	1	Seven transmembran
33	549.5	30.0	355	1	Human V28 seven tr
34	540	29.7	358	1	Sequence in a lowh
35	540	29.5	372	1	New platelet facto
36	540	29.5	372	1	Human lymphocyte p
37	540	29.5	372	1	Chemokine superfam
38	538	29.4	378	1	Epstein Barr virus
39	538	29.4	378	1	G-protein coupled
40	538	29.4	378	1	Epstein Barr virus
41	528	28.9	374	1	Human monocytic che
42	528	28.9	355	1	Human MCP-4 recept
43	527	28.8	355	1	Human G-protein re

ALIGNMENTS

44 527 28.8 355 1 W49807
45 527 28.8 342 1 W97784

Human G-protein ch
African green monk

RESULT 1
ID R68812 standard; Protein: 352 AA.
AC R68812;
DT 18-JUL-1995 (first entry)
DE Human monocytic P4AR.
KW Interleukin-8 receptor; IL-8 receptor; P4AR;
KW platelet factor superfamily receptor; monocytic; chemotactic;
KW inflammation; inflammatory disease; arthritis; emphysema; cystic;
KW fibrosis; colitis; bronchitis; meningitis; therapeutic.
OS Homo sapiens.
PN W09428931-A.
PD 22-DEC-1994.
PF 07-JUN-1994; U06380.
PR 11-JUN-1993; U076093.
PA (GETH) GENENTECH INC.
PI Chuntharapai A, Hebert C, Kim KJ, Lee J;
DR WPT: 95-036114/05.
DR N-PSDB: Q80521.
PT Treatment of inflammatory disorders - by administering an
PT antibody capable of binding a platelet factor 4 superfamily
PT receptor polypeptide
PS Disclosure: Page 54-56; 83pp; English.
CC 2 P4AR members were identified by probing lambda libraries from
CC human monocytic-like cell line HL-60 and human peripheral blood
CC lymphocytes using a large fragment of IL-8 receptor DNA (full
CC sequence given in Q80520). The nucleotide sequences of the 2
CC P4ARs are given in Q80521 and Q80522, and their respective
CC amino acid sequences in R68812 and R68813.
SQ Sequence 352 AA:

Query Match 100.0%; Score 1830; DE 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.1e-212;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGISITYSDNTEEMSGSDYSKPECPRENANFKIFLPTIYSITLTGIVNGLVI 60
|||||
DB 1 MEGISITYSDNTEEMSGSDYSKPECPRENANFKIFLPTIYSITLTGIVNGLVI 60
QY 61 LVMGVQKRLRSMTDKRYLHLISVADLLEVTLPFMVAVDAVANNYFGNLCRAHVITYVNL 120
|||||
DB 61 LVMGVQKRLRSMTDKRYLHLISVADLLEVTLPFMVAVDAVANNYFGNLCRAHVITYVNL 120
QY 121 YSSVLLAFISIDRYLAIVHATNSORPKRLAEKVVYGVWIPALLTIPDFIFANVSEA 180
|||||
DB 121 YSSVLLAFISIDRYLAIVHATNSORPKRLAEKVVYGVWIPALLTIPDFIFANVSEA 180
QY 121 YSSVLLAFISIDRYLAIVHATNSORPKRLAEKVVYGVWIPALLTIPDFIFANVSEA 180
|||||
DB 121 YSSVLLAFISIDRYLAIVHATNSORPKRLAEKVVYGVWIPALLTIPDFIFANVSEA 180
QY 181 DDRYICDRFPNDLVWVVFQFIHWGLLPGLIVILSCCIIISKLSHGQKRAKLT 240
|||||
DB 181 DDRYICDRFPNDLVWVVFQFIHWGLLPGLIVILSCCIIISKLSHGQKRAKLT 240
QY 241 TYILLAFACWLPYIGISIDSFILLEIKGCFEENVHKMISTELAFHCCLNPI 300
|||||
DB 241 TYILLAFACWLPYIGISIDSFILLEIKGCFEENVHKMISTELAFHCCLNPI 300
QY 301 LVAFLGAKFKTSAOHALTSVSRGSSSLKLSKGRGSHSVSTSESSSFHSS 352
|||||
DB 301 LVAFLGAKFKTSAOHALTSVSRGSSSLKLSKGRGSHSVSTSESSSFHSS 352
RESULT 2
ID R80757 standard; Protein: 352 AA.
AC R80757;
DT 26-MAR-1996 (first entry)

DE Chemokine superfamily receptor.
 KW Interleukin: IL-8; inflammation; psoriasis; dermatitis;
 KW rheumatoid arthritis; inflammatory bowel disease;
 KW chronic lung inflammation; treatment; antibody;
 KW affinity purification; detection.

OS Homo sapiens.

PN US5440021-A.

PD 08-AUG-1995.

PF 29-MAR-1991; 677211.

PR 29-MAR-1991; US-677211.

PA (CHUN)/ CHUNTHARAPAI A.

PA (HEBE)/ HEBERT C.

PA (KIMK)/ KIM K J.

PA (LEEJ)/ LEE J.

PI Chuntharapai A, HEBERT C, Kim KJ, Lee J;

DR WPI: 95-283151/37.

DR N-PSDB: Q29007.

PT New antibodies against interleukin 8 type B receptor - used to treat

PT or prevent inflammation, also for detecting receptor expression and

PT purification.

PS Example 2: Columns 45-48: 62pp: English.

CC Antibodies directed against the interleukin-8 receptor B can be used

CC to treat or prevent inflammation e.g. psoriasis, dermatitis,

CC rheumatoid arthritis and particularly inflammatory bowel disease and

CC chronic lung inflammation. When immobilised, these antibodies may

CC be used to detect interleukin-8 receptor B expression in cells and

CC tissues and for affinity purification of interleukin-8 receptor B

CC from cells. This sequence is an additional chemokine superfamily

CC receptor which was identified by probing lambda libraries of genomic

CC DNA from a human monocytic-like cell line (U-60) and human peripheral

CC blood lymphocytes using a large fragment of the interleukin-8 type

CC A receptor DNA (See Q29006).

SQ Sequence 352 AA:

Query Match 100.0%; Score 1830; DB 1; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.1e-212;

Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGISITSDNTEEMSGDYSKMEPCFREANFNKIFLPTIYSIFLTGIVNGLVI 60
 DB 1 MEGISITSDNTEEMSGDYSKMEPCFREANFNKIFLPTIYSIFLTGIVNGLVI 60
 QY 61 LVNGYOKKLRSMYDKYRLHLSVADLLFVITLPPWADVANNYFGNLCRAVHIYTVNL 120
 DB 61 LVNGYOKKLRSMYDKYRLHLSVADLLFVITLPPWADVANNYFGNLCRAVHIYTVNL 120
 QY 121 YSSVLLAFISLDRIYAIYHATNSQRPRLAEKVVYGVWIPALLLTIPDFIFANVSEA 180
 DB 121 YSSVLLAFISLDRIYAIYHATNSQRPRLAEKVVYGVWIPALLLTIPDFIFANVSEA 180
 QY 181 DDRYICDRFPNDLMVWVFOFHIMVGLILPGVILSCYCIILSKLSHGOKRRAKLT 240
 DB 181 DDRYICDRFPNDLMVWVFOFHIMVGLILPGVILSCYCIILSKLSHGOKRRAKLT 240
 QY 241 TVILLIAFFACWLPYYIGISIDSIFLLEIKQCEFEENTVHKWISTEALAFHCCLNPI 300
 DB 241 TVILLIAFFACWLPYYIGISIDSIFLLEIKQCEFEENTVHKWISTEALAFHCCLNPI 300
 QY 301 LVAFLGAKFETSQOHALTSVSRGSSILKLSGKRGHSSVTESESSSFHSS 352
 DB 301 LVAFLGAKFETSQOHALTSVSRGSSILKLSGKRGHSSVTESESSSFHSS 352

RESULT 3

R27792

ID R27792 standard; Protein; 352 AA.

AC R27792;

DT 12-MAR-1993 (first entry)

DE New platelet factor 4 receptor superfamily member PF4AR1.

KW IL-8; G-protein coupled receptor family; rhodopsin superfamily;

KW pro-inflammatory cytokine; 8tr.20.15.

OS Homo sapiens.

PN W09217497-A.

PD 13-OCT-1992.

PF 23-MAR-1992; U02317.

PR 29-MAR-1991; US-677211.

PA (GETH) GENENTECH INC.

PA Holmes WE, Lee J, Wood WI;

PI WPI: 92-366191/44.

DR N-PSDB: Q29506.

PT Isolated human platelet factor 4 super-family receptor

PT polypeptide and corresp. antibodies and DNA - useful as

PT diagnostic and screening agents, and for treating inflammation or

PT PF4AR-mediated disorders

PS Claim 7: Fig 4: 78pp: English.

CC The IL-8 receptor cDNA sequence was isolated (see Q29505) and a

CC 874bp sub-fragment of the coding sequence was used as a probe to

CC screen human cell line HL60 and human peripheral blood lymphocyte

CC cDNA libraries. Two new gene sequences were found that are clearly

CC related to the IL-8 receptor. One of these was contained in

CC combined clone 8tr.20.15 and is predicted to encode an amino acid

CC sequence which is 34% identical with both the high and low affinity

CC IL-8 receptors. See also Q37107.

SQ Sequence 352 AA:

Query Match 99.4%; Score 1819; DB 1; Length 352;

Best Local Similarity 99.7%; Pred. No. 4.5e-211;

Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEGISITSDNTEEMSGDYSKMEPCFREANFNKIFLPTIYSIFLTGIVNGLVI 60
 DB 1 MEGISITSDNTEEMSGDYSKMEPCFREANFNKIFLPTIYSIFLTGIVNGLVI 60
 QY 61 LVNGYOKKLRSMYDKYRLHLSVADLLFVITLPPWADVANNYFGNLCRAVHIYTVNL 120
 DB 61 LVNGYOKKLRSMYDKYRLHLSVADLLFVITLPPWADVANNYFGNLCRAVHIYTVNL 120
 QY 121 YSSVLLAFISLDRIYAIYHATNSQRPRLAEKVVYGVWIPALLLTIPDFIFANVSEA 180
 DB 121 YSSVLLAFISLDRIYAIYHATNSQRPRLAEKVVYGVWIPALLLTIPDFIFANVSEA 180
 QY 181 DDRYICDRFPNDLMVWVFOFHIMVGLILPGVILSCYCIILSKLSHGOKRRAKLT 240
 DB 181 DDRYICDRFPNDLMVWVFOFHIMVGLILPGVILSCYCIILSKLSHGOKRRAKLT 240
 QY 241 TVILLIAFFACWLPYYIGISIDSIFLLEIKQCEFEENTVHKWISTEALAFHCCLNPI 300
 DB 241 TVILLIAFFACWLPYYIGISIDSIFLLEIKQCEFEENTVHKWISTEALAFHCCLNPI 300
 QY 301 LVAFLGAKFETSQOHALTSVSRGSSILKLSGKRGHSSVTESESSSFHSS 352
 DB 301 LVAFLGAKFETSQOHALTSVSRGSSILKLSGKRGHSSVTESESSSFHSS 352

RESULT 4

W97362

ID W97362 standard; Protein; 356 AA.

AC W97362;

DT 12-MAY-1999 (first entry)

DE G-protein coupled receptor polypeptide designated CXCR4B.

KW G-protein coupled receptor; CXCR4B; human; splice variant;

KW chemokine receptor; CXCR4; vaccine; gene therapy; HIV-1; HIV-1;

KW cancer; pain; diabetes; obesity; anorexia; bulimia; asthma;

KW Parkinson's disease; acute heart failure; hypotension; hypertension;

KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;

KW stroke; ulcer; allergy; benign prostatic hyper trophy; migraine;

KW vomiting; psychotic disorder; neurological disorder; anxiety;

KW schizophrenia; manic depression; delirium; dementia; mental retardation;

KW dyskinesias; Huntington's disease; Gilles de la Tourette syndrome.

OS Homo sapiens.

PN EP-897980-A2.

PD 24-FEB-1999.

R53753
ID R53753 standard; Protein: 337 AA.
AC R53753:
DT 07-FEB-1995 (first entry)
DE Seven transmembrane receptor (RM3).
KW Primer: seven transmembrane receptor; receptor; amplification; PCR;
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 48..69
FT domain /label= Transmembrane domain.
FT domain 82..100
FT domain /label= Transmembrane domain.
FT domain 115..136
FT domain /label= Transmembrane domain.
FT domain 159..179
FT domain /label= Transmembrane domain.
FT domain 198..220
FT domain /label= Transmembrane domain.
FT domain 246..274
FT domain /label= Transmembrane domain.
FT domain 287..311
FT domain /label= Transmembrane domain.
FT domain /label= Transmembrane domain.
PN WO9412635-A.
PD 09-JUN-1994.
PF 17-NOV-1993; U11153.
PR 17-NOV-1992; US-977452.
PA (ICOS-) ICOS CORP.
PI Godiska R, Gray PW, Schwelckart VL;
DR WPI: 94-200264/24.
DR N-PSDB: Q66179.
PT DNA encoding seven transmembrane receptors - used to develop
PT prod. for use as therapeutic or diagnostic agents for conditions
PT involving the receptors.
PS Example 11: Pages 84-85; 100pp; English.
CC Two primers (Q66148, Q66149) were used in a PCR reaction containing
CC human macrophage cDNA library in plasmid pRC/CMV. When the PCR
CC products were subjected to agarose gel electrophoresis a faint band
CC of 180-200 base pairs was observed. Re-amplified material was
CC digested with BamHI and HindIII and cloned into the plasmid
CC Bluescript SK-. Of sixteen clones sequenced, two contained a unique
CC sequence termed RM3. Specific primers for the partial RM3 clone were
CC used to identify a full length RM3 cDNA clone (Q66179) which
CC encoded this seven transmembrane receptor.
SQ Sequence 337 AA:

Query Match 95.2%; Score 1742; DB 1; Length 337;
Best Local Similarity 99.7%; Pred. No. 8.2e-202;
Matches 336; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 MGSDDVSMKEPCFRENANFNKIFPTIYSIFLNGIVNGVILVMGYOKRLRSWTDK 75
DB 1 MGSDDVSMKEPCFRENANFNKIFPTIYSIFLNGIVNGVILVMGYOKRLRSWTDK 60
QY 76 YRLHLVSADLLFYITLPEFNAVDAVAMNVEGNFLCKAVHYITVNLXSSVLLAFISIDRY 135
DB 61 YRLHLVSADLLFYITLPEFNAVDAVAMNVEGNFLCKAVHYITVNLXSSVLLAFISIDRY 120
QY 136 LAIVHATNSORPKLLAEKVVYVGVWIPALLLTIPDFIFANVSEADRYICDRFPNDLW 195
DB 121 LAIVHATNSORPKLLAEKVVYVGVWIPALLLTIPDFIFANVSEADRYICDRFPNDLW 180
QY 196 VVYFQFOHIMVGLIPGIVILSCYCIISKLNSKHOKRAKATYVILLAFACMLPY 255
DB 181 VVYFQFOHIMVGLIPGIVILSCYCIISKLNSKHOKRAKATYVILLAFACMLPY 240
QY 256 YIGISIDSFLLLEIKOGCEFEFNTVHKWISTEALAFHCCNLPITYAFIAGAKFISAOH 315
DB 241 YIGISIDSFLLLEIKOGCEFEFNTVHKWISTEALAFHCCNLPITYAFIAGAKFISAOH 300
QY 316 ALTSVSRGSSSLKILSKGRGSHSVSTESSSPFHS 352
DB 316 ALTSVSRGSSSLKILSKGRGSHSVSTESSSPFHS 352

DB 301 ALTSVSRGSSSLKILSKGRGSHSVSTESSSPFHS 337
RESULT 7
W64778
ID W64778 standard; Protein: 359 AA.
AC W64778:
DT 20-NOV-1998 (first entry)
DE A murine CXC chemokine receptor.
KW Mouse; CXC chemokine receptor; pre-B cell line DW34;
KW CXC chemokine pre-B cell stimulatory factor PBSF/SDF-1;
KW HIV infection; screening; inhibitor; AIDS.
OS Mus sp.
PN WO9835035-A1.
PD 13-AUG-1998.
PF 07-FEB-1997; J00299.
PR 07-FEB-1997; WO-J00299.
PA (SHO) SHIONOGI & CO LTD.
PI Iizasa H, Kishimoto T, Nagasawa T, Nakajima T, Tachibana K,
PI Yoshida N, Yoshie O;
DR WPI: 98-447232/38.
DR N-PSDB: V46370.
PT Mouse CXC chemokine receptor binding to PBSF/SDF-1 pre-B cell
PT stimulatory factor - is useful for screening of potential HIV
PT infection and AIDS inhibitors
PS Claim 1: Pages 54-56; 76pp; Japanese.
CC The present sequence represents a murine CXC chemokine receptor which
CC binds to the mouse CXC chemokine pre-B cell stimulatory factor
CC PBSF/SDF-1. The nucleic acid is isolated from mouse pre-B cell
CC line DW34. The receptor and cells expressing it can be used in the
CC study and mapping of the mechanism of HIV infection and in screening
CC of potential inhibitors of HIV infection and the development of AIDS.
SQ Sequence 359 AA:

Query Match 91.7%; Score 1678.5; DB 1; Length 359;
Best Local Similarity 90.1%; Pred. No. 4.1e-194;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

QY 4 ISIVTSDNTEMGSDVSMKEPCFRENANFNKIFPTIYSIFLNGIVNGVILVM 63
DB 6 VSVTSDNTEMGSDVSMKEPCFRENANFNKIFPTIYSIFLNGIVNGVILVM 65
QY 64 GYOKRLRSMTDXYRLHLVSADLLFYITLPEFNAVDAVAMNVEGNFLCKAVHYITVNLXSS 123
DB 66 GYOKRLRSMTDXYRLHLVSADLLFYITLPEFNAVDAVAMNVEGNFLCKAVHYITVNLXSS 125
QY 124 VLLAFISIDRYLAIVHATNSORPKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178
DB 126 VLLAFISIDRYLAIVHATNSORPKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 185
QY 179 EADDRICORFYPNDLWVYFQFOHIMVGLIPGIVILSCYCIISKLNSKHOKRAK 238
DB 186 QGDRIICORLPDLSVMVYFQFOHIMVGLIPGIVILSCYCIISKLNSKHOKRAK 245
QY 239 KTTVILLAFACMLPYIYIGISIDSFILLEIKOGCEFEFNTVHKWISTEALAFHCCN 298
DB 246 KTTVILLAFACMLPYIYIGISIDSFILLEIKOGCEFEFNTVHKWISTEALAFHCCN 305
QY 299 PIIYAFIAGAKFISAOHALTSVSRGSSSLKILSKGRGSHSVSTESSSPFHS 352
DB 306 PIIYAFIAGAKFISAOHALTSVSRGSSSLKILSKGRGSHSVSTESSSPFHS 359

RESULT 8
R99274
ID R99274 standard; Protein: 360 AA.
AC R99274:
DT 09-DEC-1996 (first entry)
DE Chemokine receptor K5.5.
KW Chemokine receptor K5.5; MIP-1-alpha; RANTES; MCP-1; allergy;
KW atheroma; HIV; AIDS; graft rejection; stem cell.
OS Homo sapiens.

PN W09623068-A1.
 PD 01-AUG-1996.
 PF 24-JAN-1996: G00143.
 PR 27-JAN-1995: GB-001683.
 PA (GLAXO) GLAXO GROUP LTD.
 PI Power CA, Wells TNC.
 DR WPI: 96-362692/36.
 DR N-PSDB: T35277.
 DR Chemokine receptor which binds MIP-1-alpha, RANTES and/or MCP-1 -
 PT useful in screening for agents to treat asthma, hay fever, eczema,
 PT allergies, atopic dermatitis, rhinitis or conjunctivitis.
 PS Claim 1: Fig 3: 47pp: English.
 CC Human chemokine receptor K5.5 (R99274) binds MIP-1-alpha, RANTES
 CC and/or MCP-1. Its amino acid sequence was deduced from a cDNA
 CC clone (T35277) obtd. from a human spleen lambda g11 cDNA
 CC library. Recombinant chemokine receptor K5.5 can be expressed
 CC in transfected host cells. It can be used to screen for agents
 CC which act as antagonists to MCP-1, MIP-1-alpha and/or RANTES.
 CC Such agents may be useful in treating allergies, atherosclerosis
 CC diseases mediated by viruses, such as AIDS. They can also be
 CC used to prevent graft rejection or to protect stem cells from
 CC the effects of chemotherapy.
 CC Sequence 360 AA:
 SQ
 Query Match 32.7%; Score 597.5; DB 1: Length 360;
 Best Local Similarity 39.4%; Pred. No. 1.1e-63;
 Matches 115; Conservative 61; Mismatches 113; Indels 3; Gaps 2;
 QY 21 YDSMKRCPREANFNKIFLPTIYSIFLTGIVNGVILVMGYOKLRKSTKTRHL 80
 DB 22 YESIPRCCKEGKAGELPLPLVSLVFGILGNSVYVLLFFYKRLKSTMDVLLNL 81
 QY 81 SVADLLFVITLPWAVDAVANNYFGNFKAVHYITVNLVSSVLLAFISDRYLAIV 140
 DB 82 AISDLLFVSLPFWGYADQWVFGGLCKMISMTLVFGISGFVPMAMSDRYLAIV 141
 QY 141 ATMSORPKLAEKVVYGVWIPALLITPDPFANVSEADRYICDRFP--NDLWVYV 198
 DB 142 AVTSRLRITLYGVITSLAVSAVFPASLPGLFSTCYERNHTYCKTYSINSTWKL 201
 QY 199 FOFQHNWGLIPGIVILSCYCIISKLSKQKRAKTKTVILLAFACMLPYTIG 258
 DB 202 SSELINILGVIPGLIMFCYSMAITLQCKNEKNKRAVMAFVAVVFLGWTGYNYV 261
 QY 259 ISDSFILLEIKQCEFEENVHKWISITTEALAFHCCCLNPIDYAFGAKF 310
 DB 262 LLELVELEV--QDCTFERLDVAIAOTETLAFVHCCLNPIDYFEGEKR 312
 RESULT 9
 W69999 standard: Protein: 367 AA.
 ID W69999: standard: Protein: 367 AA.
 AC 20-OCT-1998 (first entry)
 DE Rodent chemokine receptor HST01.1 amino acid sequence.
 KW Chemokine; primate; human; rodent; chemokine receptor; asthma;
 KW inflammatory response; immune response; leukocyte migration; GPCR;
 KW leukocyte adhesion; chemottractant; modulation; antiviral response;
 KW cellular morphology modification; abnormal proliferation; regeneration;
 KW phosphoinositide lipid turnover; abnormal proliferation; regeneration;
 KW atrophy; HST01.1.
 OS Mus sp.
 OS W09832858-A2.
 PD 30-JUL-1998.
 PF 22-JAN-1998: U00902.
 PR 23-JAN-1997: US-036715.
 PA (SCHE) SCHERING CORP.
 PI Gorman DM, Hedrick JA, Mattison JD, Soto-trejo H,
 PI Zlotnik A,
 DR WPI: 98-427954/36.
 DR N-PSDB: V43793.
 PT Rodent and primate chemokines and chemokine receptors - useful

PT diagnostically and therapeutically to treat conditions associated
 PT with abnormal physiology or development e.g. inflammatory conditions
 PS Claim 4: Pages 89-92: 105pp: English.
 CC This represents a rodent chemokine receptor HST01.1 amino acid sequence.
 CC The invention provides novel primate and rodent chemokines and chemokine
 CC receptors. The chemokines, receptors and binding compounds (optionally
 CC antibodies/fragments specifically binding the chemokines) are useful
 CC therapeutically to treat conditions associated with abnormal physiology
 CC or development e.g. inflammatory conditions such as asthma. Chemokines
 CC are important in immune and inflammatory responses in that they induce
 CC leukocyte migration and adhesion. They are also chemottractants for
 CC several cells involved in inflammation and can induce other biological
 CC responses e.g. modulation of second messenger levels (e.g. Ca²⁺),
 CC cellular morphology modification responses etc. The chemokine receptors of
 CC turnover, possible antiviral responses etc. The chemokine receptors of
 CC the invention exhibit structural properties of G-protein coupled
 CC receptors (GPCR), although their ligands have not yet been identified.
 CC The chemokine and chemokine receptor polypeptides are useful to produce
 CC ligand/receptor complexes in vivo or in assay techniques. Assays may
 CC also involve chemical antagonists which block complex production or
 CC utilize competitive binding. Binding compounds identified (agonists or
 CC antagonists) can be used to modulate the physiological responses in cells
 CC (especially neurons, macrophages or lymphocytes) to treat e.g. abnormal
 CC proliferation, regeneration, generation and atrophy. The polypeptides
 CC are also used to produce antibodies useful diagnostically, for drug
 CC screening or for polypeptide purification. The polynucleotides are useful
 CC to produce probes for detecting the polypeptides, and to isolate the
 CC polypeptides or related sequences, especially from other species. They
 CC also allow transformation of cells for polypeptide production.
 SQ Sequence 367 AA:
 Query Match 31.6%; Score 578; DB 1: Length 367;
 Best Local Similarity 35.3%; Pred. No. 2.6e-61;
 Matches 120; Conservative 71; Mismatches 133; Indels 16; Gaps 6;
 QY 15 EMGSGDYD-SMKRCPREANFNKIFLPTIYSIFLTGIVNGVILVMGYOKLRKST 73
 DB 28 DYGENESDFSDSPDQDFSLNDFRLPALVSLFLDLGLGAVAAVLLQORALST 87
 QY 74 DKYRLHSVADLLFVITLPWAVDAVANNYFGNFKAVHYITVNLVSSVLLAFISD 133
 DB 88 DFLHLAVADVLLVITLPWAVDAVANNYFGNFKAVHYITVNLVSSVLLAFISD 147
 QY 134 RYLAIVANTNSQ--PKLLAEKVVYGVWIPALLITPDPF--ANVSEADRYICDF 189
 DB 148 RYLSIVHATQYRDPVRAV--LTCIVWGILCLRALPFIYLSANYDORLNATQCN 205
 QY 190 YPNDLWVYVFOFHIMGLIPGIVILSCYCIISKLSKQKRAKTKTVILLAF 249
 DB 206 FP-QVGRALNVDQVAGFLPLVMAVCYAHILAVLVYRGQRFRMRLLVYVVAFA 264
 QY 250 ACMLPYTIGISDSFILLEIKQCEFEENVHKWISITTEALAFHCCCLNPIDYAFGAKF 309
 DB 265 VCMTPFHLVYVDLIMDGVILARNCGKSHVDAKSVTSGVYHCCCLNPIDYAFYVKF 324
 QY 310 KTSQAHALTSVGRSSKLLSKGKRGHSSVSTSESSSF 349
 DB 325 REKMMMLFTRIGSD-----QNGPORPSSSRRESSW 356
 RESULT 10
 W54371 standard: Protein: 368 AA.
 ID W54371: standard: Protein: 368 AA.
 AC 14-AUG-1998 (first entry)
 DE Human IP-10/Mig receptor CXCR3 protein.
 KW chemokine receptor; cellular signal; treatment; T cell; antitumor;
 KW antiviral; inflammatory disease.
 OS Homo sapiens.
 OS Key location/Qualifiers
 FT Modified site 22
 FT /note="N-linked glycosylation site"

FT Modified_site 32
 /note= "N-linked glycosylation site"
 FT Domain 59..79
 /note= "TM1 transmembrane domain"
 FT Domain 91..111
 /note= "TM2 transmembrane domain"
 FT Domain 127..147
 /note= "TM3 transmembrane domain"
 FT Domain 170..190
 /note= "TM4 transmembrane domain"
 FT Modified_site 199
 /note= "N-linked glycosylation site"
 FT Domain 224..244
 /note= "TM5 transmembrane domain"
 FT Domain 257..277
 /note= "TM6 transmembrane domain"
 FT Domain 302..322
 /note= "TM7 transmembrane domain"
 PN WO9811218-A1.
 PD 19-MAR-1998.
 PE 10-SEP-1997; US5915.
 PR 31-MAR-1997; US-829839.
 PR 10-SEP-1996; US-709838.
 PA (KOECH-) KOECHER INST THEODOR.
 PI (LEUK-) LEUKOSITE INC.
 PI Loetscher M, Mackay CR, Moser B, Qin S;
 DR WPI: 98-207381/18.
 DR N-PSDB: V26557.
 PT DNA encoding CXCR3 chemokine receptor 3 - inhibitors and promoters of
 PT which, are useful for treatment of inflammation or in anti-tumour or
 PT anti-viral therapy.
 PS Claim 7; Fig 2; 137pp; English.
 CC The mammalian CXCR3 chemokine receptor 3 (CXCR3) protein can selectively
 CC bind one or more chemokines and can mediate cellular signalling and/or a
 CC cellular response in response. Inhibitors and promoters of mammalian
 CC CXCR3 can be detected and identified using host cells expressing CXCR3.
 CC CXCR3 inhibitors can be used for treatment of inflammatory diseases which
 CC are T cell mediated. CXCR3 promoters are useful for antitumour or
 CC antiviral therapy.
 SO Sequence 368 AA:

Query Match 31.5%; Score 576.5; DB 1; Length 368;
 Best Local Similarity 35.0%; Pred. No. 4e-61;
 Matches 121; Conservative 70; Mismatches 140; Indels 15; Gaps 4;

QY 10 DNTTEMGSGDDYS---MKPCRENNANFKIPLTYISITFLGIVNGVILVMGY 65
 DB 21 ENFSSSYDYENESDSCCTSPCPDPSLNFDRAPLALYSLLFLGLGNGAVAAVLLS 80
 QY 66 OKKLRMTDXYRLHLVADLLEVTLPFMAVDVAVMYFGNFKCAVHYITVNLKSYVL 125
 DB 81 RRRLASTDTFLHLNADLVLPVLMVADAVQVWESSGLCKAGALFNFTAGAL 140
 QY 126 ILAFISIDRYLAIVHAATNSORPKLLAEKVYVGVWIPALLTTPDPIF--ANVSEADR 183
 DB 141 LLAACISDFRILNIVHATOLRRSPARAVTLTCLAVMGLCLFALPDPFIPLSAHDESLNA 200
 QY 184 YICDRFPNDLVWVFOFOHIMGLIPGVILSCYIIISKSHSGHGRKRAKLTIVY 243
 DB 201 THCOYVNP--OVGRATLAVQLVAGFLLPLVMVVCYAHILAVLVSSGQRLAMRLVYV 259
 QY 244 LILAFACWLPYVIGISIDSFILLEIKOCCEFFENVHKWISTEALAFHCCINPLIYA 303
 DB 260 VVAFALCWTPYHLVAVLIDMLGALARNCGRESRVDVAKSVTSGLGVNHCCLNPLIYA 319
 QY 304 FLGAKRTSAQHALTSVSRGSSSKILSKRGHSHSVSTESSESSF 349
 DB 320 FVGKFREREMMLL-----LRLGCPNQRGLQROPSSSRDSSW 357

RESULT 11
 R80953

ID R80953 standard; Protein; 360 AA.
 AC R80953;
 DT 24-APR-1996 (first entry)
 DE Recombinant high affinity interleukin-8 receptor subtype B.
 KW IL-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder;
 KW anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis;
 KW adult respiratory distress syndrome; psoriasis; asthma; allergy; ARDS;
 OS Homo sapiens.
 PN WO9525126-A1.
 PD 21-SEP-1995.
 PE 09-MAR-1995; US03032.
 PR 15-MAR-1994; US-210250.
 PR 02-MAY-1994; US-237937.
 PA (REPK) REPLIGEN CORP.
 PA (UYRO-) UNITV BOSTON.
 PI Greenfield EA, Larosa GJ, Navarro J, Thomas KM;
 PI Wilt DT;
 DR WPI: 95-336945/43.
 DR N-PSDB: Q99952.
 PT Monoclonal antibody against recombinant IL-8 receptor polypeptide -
 PT useful for treating inflammatory disorders, for detecting
 PT neutrophil(s) and for isolating IL-8 receptor from liq.mxt.
 PS Claim 5; Fig 4A-B; 74pp; English.
 CC Monoclonal antibodies were raised against recombinant interleukin-8
 CC (IL-8) receptor subtypes A and B from both human and rabbit sources
 CC (R80950-53 encoded by Q9949-52). The A subtype receptor (IL-8RA) is
 CC a high affinity receptor and the B subtype receptor (IL-8RB) is a
 CC low affinity receptor. The monoclonal antibody (mAb) pret. binds to
 CC the IL-8 binding domain thus blocking its activation. The mAbs are
 CC useful for treating inflammatory disorders (see key words) and for
 CC detecting the presence of neutrophils in a biological sample. The
 CC mAbs are also useful in the isolation of IL-8 receptors from a mixture.
 SO Sequence 360 AA:

Query Match 31.4%; Score 574; DB 1; Length 360;
 Best Local Similarity 35.6%; Pred. No. 7.8e-61;
 Matches 133; Conservative 67; Mismatches 120; Indels 54; Gaps 11;

QY 9 SDNYT-----EEMSGGDDSM-----KEPCRENNANFKIPLTYISITFLGIVGN 56
 DB 8 DSFDEPMKGEDLSNYSYSTLPPLDAPC-EPESLEINKYFVYIYALVFLSLIGN 66
 QY 57 GVLIVMGYOKRLMTDXYRLHLVADLLEVTLPFMAVDVAVMYFGNFKCAVHYIY 116
 DB 67 SLVMLYILSKRGSRVTVYILNLAIDLPLALITPIPAASVNVNMTGTRCKVSLIK 126
 QY 117 TVNLYSSVILAFISIDRYLAIVHAATNSORPKLLAEKVYVGVWIPALLTTPDPIFA- 176
 DB 127 ENFYSGLILLACISVDRLAIVHAATRLTQKAYLV-KFICLSIWWLSLALPVLPAR 185
 QY 176 -----NVSADRYICDRFPNDL--WVYVFOFOHIMGLIPGVILSCYIIISKSH 228
 DB 186 TYSSNVSPA-----CYEDMGNTNANMALLAIIPQSEGFIVPLIMFCYGFTRTLTK 240
 QY 229 SKGHORRKLKTTVTLILAFACWLPYVIGISIDSFILLEIKOCCEFFENVHKWISTE 288
 DB 241 AHMGKRRMARVYFAVVLFLCWLPRYNVYLADILMTKTYQIQCERNRHNDRADLDATE 300
 QY 289 ALAFHCCINPLIYAFLGAKRTSAQHALTSVSRGSSSKILSKRGHSHSVSTESSESSF 345
 DB 301 ILGILHSCNPLIYAFIGQKFR-----HGLV-----LKLIAL-----HGLISKDSLPRD 343
 QY 345 -----ESSFHS 352
 DB 344 SRPSFVSSSGHTS 357

RESULT 12
 R70124
 ID R70124 standard; Protein; 1064 AA.
 AC R70124;


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OY 421 GCAGTCATGTCATCTACACAGTCACCTCTACAGCAGTGTCTCATCCGCGCCCTCATC 480
    |||||||
Db 421 GCAGTCATGTCATCTACACAGTCACCTCTACAGCAGTGTCTCATCCGCGCCCTCATC 480
OY 481 AGTCTGAGCGGTACCTGGCCATGTCACAGCCACCAAGTCAGAGGCCAAGAAGCTG 540
    |||||||
Db 481 AGTCTGAGCGGTACCTGGCCATGTCACAGCCACCAAGTCAGAGGCCAAGAAGCTG 540
OY 541 TTGGCTGAAAAGGTGTCTATGTTGGCGTCTGATCCCTGGCCCTCTGGCTGACTATCC 600
    |||||||
Db 541 TTGGCTGAAAAGGTGTCTATGTTGGCGTCTGATCCCTGGCCCTCTGGCTGACTATCC 600
OY 601 GACTTATCTTTGCCAAGTCAGTGAAGCAGATGATATATCTGTGACCGCTTCTAC 660
    |||||||
Db 601 GACTTATCTTTGCCAAGTCAGTGAAGCAGATGATATATCTGTGACCGCTTCTAC 660
OY 661 CCCAATGACTTGTGGTGTGTGTTCCAGTTTCAGACATCATGTTGGCCCTTATCTG 720
    |||||||
Db 661 CCCAATGACTTGTGGTGTGTGTTCCAGTTTCAGACATCATGTTGGCCCTTATCTG 720
OY 721 CCTGTATGTCTATCTCTGTCCTCTATGATATATCATCTCCAAAGTGTACACTCCAG 780
    |||||||
Db 721 CCTGTATGTCTATCTCTGTCCTCTATGATATATCATCTCCAAAGTGTACACTCCAG 780
OY 781 GGGCAGCAGAGGCGCAAGGCCCTCAAGACCAAGTCATCTCTGCTGCTTCTTCCGCC 840
    |||||||
Db 781 GGGCAGCAGAGGCGCAAGGCCCTCAAGACCAAGTCATCTCTGCTGCTTCTTCCGCC 840
OY 841 TGTGTGCTGCTTACTACATATGGGATCAGCATGACTCTCTCATCTCTGCTGCTGCT 900
    |||||||
Db 841 TGTGTGCTGCTTACTACATATGGGATCAGCATGACTCTCTCATCTCTGCTGCTGCT 900
OY 901 AAGCAAGGGGTAGTGTGGAACACTGTGCACAAAGTGGATTCACACGAGGCCCTA 960
    |||||||
Db 901 AAGCAAGGGGTAGTGTGGAACACTGTGCACAAAGTGGATTCACACGAGGCCCTA 960
OY 961 GCTTCTTCACATGTTGTCTGAAGCCCATCTCTATGCTTCTGAGGCCAATTTAA 1020
    |||||||
Db 961 GCTTCTTCACATGTTGTCTGAAGCCCATCTCTATGCTTCTGAGGCCAATTTAA 1020
OY 1021 ACCTGTGCCAGCAGCAGCTACCTCTGTGAGCAGAGGGTCCAGCTCAAGTCTCTCC 1080
    |||||||
Db 1021 ACCTGTGCCAGCAGCAGCTACCTCTGTGAGCAGAGGGTCCAGCTCAAGTCTCTCC 1080
OY 1081 AAGGAAAGGAGGTGACATCTGTTCCAGTGAAGTCTCAAGTCTTCAAGTCTTCC 1140
    |||||||
Db 1081 AAGGAAAGGAGGTGACATCTGTTCCAGTGAAGTCTCAAGTCTTCAAGTCTTCC 1140
OY 1141 TCCAGCTAACACAGATGTAAGACCTTTTATAGATAAATTAATCTTTTAAAGT 1200
    |||||||
Db 1141 TCCAGCTAACACAGATGTAAGACCTTTTATAGATAAATTAATCTTTTAAAGT 1200
OY 1201 ACACATTTTTCAGATATAAAGACTGACCAATATGTTACAGTTTATGCTGTTGAT 1260
    |||||||
Db 1201 ACACATTTTTCAGATATAAAGACTGACCAATATGTTACAGTTTATGCTGTTGAT 1260
OY 1261 TTTTGTCTGTGTCTTCTTGTGTTTGTGAAGTTTAATTAATTAATTAATTTT 1320
    |||||||
Db 1261 TTTTGTCTGTGTCTTCTTGTGTTTGTGAAGTTTAATTAATTAATTAATTTT 1320
OY 1321 TTTTGTTCATATGATGTGTGTCTAGCAGAGCTGTGGCAAGTCTTGTGCTGAT 1380
    |||||||
Db 1321 TTTTGTTCATATGATGTGTGTCTAGCAGAGCTGTGGCAAGTCTTGTGCTGAT 1380
OY 1381 GTCTCGTGTAGAGCTGTAGAAAAGGAACTGAACATTCAGAGCGGTAGTGAATCAG 1440
    |||||||
Db 1381 GTCTCGTGTAGAGCTGTAGAAAAGGAACTGAACATTCAGAGCGGTAGTGAATCAG 1440
OY 1441 TAAAGTAGAATATGATCCCAAGCTGTTATGATAGATAATCTCTCATTCCTGCTGAG 1500
    |||||||
Db 1441 TAAAGTAGAATATGATCCCAAGCTGTTATGATAGATAATCTCTCATTCCTGCTGAG 1500

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OY 1501 GTTTTCTGTTCTTAAAGCAGTATTTGCTGTAGAGATGACACTTAAACAAAGCC 1560
    |||||||
Db 1501 GTTTTCTGTTCTTAAAGCAGTATTTGCTGTAGAGATGACACTTAAACAAAGCC 1560
OY 1561 AAAGTGTATAGAAATGCTGTTTTCAGTTTTCAGAGTGGGTTGATTACGACCTAC 1620
    |||||||
Db 1561 AAAGTGTATAGAAATGCTGTTTTCAGTTTTCAGAGTGGGTTGATTACGACCTAC 1620
OY 1621 AGTTCAGCTCTGTATATAGTGTATTAATAAGTACATGTTAACTTAAAAA 1680
    |||||||
Db 1621 AGTTCAGCTCTGTATATAGTGTATTAATAAGTACATGTTAACTTAAAAA 1680
OY 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCAGCAGCAGTGAATTC 1737
    |||||||
Db 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCAGCAGCAGTGAATTC 1737

RESULT 2
ID 099007 standard; cDNA; 1737 bp.
AC 099007:
DT 26-MAR-1996 (first entry)
DE Chemokine superfamily receptor coding sequence.
KW Interleukin; IL-8; inflammation; psoriasis; dermatitis;
KW rheumatoid arthritis; inflammatory bowel disease;
KW chronic lung inflammation; treatment; antibody;
KW affinity purification; detection; ss.
OS Homo sapiens.
PN US3440021.A.
PD 08-AUG-1995.
PF 29-MAR-1991; 677211.
PR 29-MAR-1991; US-677211.
PR 25-FEB-1994; US-202056.
PA (CHUN/) CHUNTHARAPAI A.
PA (HEBE/) HEBERT C.
PA (KIM/) KIM K J.
PA (LEE/) LEE J.
PA Chuntharapai A. Hebert C, Kim KJ, Lee J;
PI MPI: 95-283151/37.
DR P-PSDB: R80757.
PT New antibodies against interleukin 8 type B receptor - used to treat
PT or prevent inflammation, also for detecting receptor expression and
PT purification.
PS Example 2: Columns 47-50; 62pp; English.
CC Antibodies directed against the interleukin-8 receptor B can be used
CC to treat or prevent inflammation e.g. psoriasis, dermatitis,
CC rheumatoid arthritis and particularly inflammatory bowel disease and
CC chronic lung inflammation. When immobilised, these antibodies may
CC be used to detect interleukin-8 receptor B expression in cells and
CC tissues and for affinity purification of interleukin-8 receptor B
CC from cells. This sequence is an additional chemokine superfamily
CC receptor which was identified by probing lambda libraries of genomic
CC DNA from a human monocyte-like cell line (L-60) and human peripheral
CC blood lymphocytes using a large fragment of the interleukin-8 type
CC A receptor DNA (see Q99006).
SQ Sequence 1737 bp; 454 A; 411 C; 373 G; 499 T;

Query Match 100.0%; Score 1737; DB 1; Length 1737;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1737; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAATTCAGTGTGCTGGCGCGCGCGCAAGTGAACGCGAGGCGCTGAGTCTCAGTA 60
    |||||||
Db 1 GAATTCAGTGTGCTGGCGCGCGCGCAAGTGAACGCGAGGCGCTGAGTCTCAGTA 60
OY 61 GCCACGCACTCTGAGAAACACAGCGTTACATGAGAGGGATCAGTATATACACTTCAGAT 120
    |||||||
Db 61 GCCACGCACTCTGAGAAACACAGCGTTACATGAGAGGGATCAGTATATACACTTCAGAT 120
OY 121 AACTACCCGAGAAATGGGCTCAGGGGCACTATGACTCCATGAGAAACCTGTTCCGT 180
    |||||||
Db 121 AACTACCCGAGAAATGGGCTCAGGGGCACTATGACTCCATGAGAAACCTGTTCCGT 180

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QY 181 GAAGAAATGTAATTCATTAATAATCTTCTGCGCAACATCTACATCATCTTCTTA 240
 DB 181 GAAGAAATGTAATTCATTAATAATCTTCTGCGCAACATCTACATCATCTTCTTA 240
 QY 241 ACTGGCATTTGGGCAATGATGGTTCATCCTGGTTCATGGTTACGAAAGAACTGAGA 300
 DB 241 ACTGGCATTTGGGCAATGATGGTTCATCCTGGTTCATGGTTACGAAAGAACTGAGA 300
 QY 301 AGCATGACGACAGTACAGGCTGACCTGTCACTGGCCGACCTCTCTTTGTCACG 360
 DB 301 AGCATGACGACAGTACAGGCTGACCTGTCACTGGCCGACCTCTCTTTGTCACG 360
 QY 361 CTTCCTCTTGGGCAATGATGGTTCATCCTGGTTCATGGTTACGAAAGAACTGAGA 420
 DB 361 CTTCCTCTTGGGCAATGATGGTTCATCCTGGTTCATGGTTACGAAAGAACTGAGA 420
 QY 421 GCATGCTATGATCTACAGAGTCAACCTGTACAGAGTGTCTCATCTGGCTTCTATC 480
 DB 421 GCATGCTATGATCTACAGAGTCAACCTGTACAGAGTGTCTCATCTGGCTTCTATC 480
 QY 481 AGTGTGACCGCTACCTGGCCATGTCACGCGCAACAGTCAAGTCCAGAGGAGAGCTG 540
 DB 481 AGTGTGACCGCTACCTGGCCATGTCACGCGCAACAGTCAAGTCCAGAGGAGAGCTG 540
 QY 541 TTGGCTGAAAGGCTGATGTTGGGCTGATCCCTGGCTGATCCCTGATCTATCC 600
 DB 541 TTGGCTGAAAGGCTGATGTTGGGCTGATCCCTGGCTGATCCCTGATCTATCC 600
 QY 601 GACTTCATCTTGGCAACGTCAGTGAAGGAGATGATATATCTGTGACCGGTTCTAC 660
 DB 601 GACTTCATCTTGGCAACGTCAGTGAAGGAGATGATATATCTGTGACCGGTTCTAC 660
 QY 661 CCCATGCTGTTGGGCTGATGTTGGGCTGATCCCTGGCTGATCCCTGATCTATCC 720
 DB 661 CCCATGCTGTTGGGCTGATGTTGGGCTGATCCCTGGCTGATCCCTGATCTATCC 720
 QY 721 CCTGATGATGATCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 780
 DB 721 CCTGATGATGATCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 780
 QY 781 GGGCACCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
 DB 781 GGGCACCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
 QY 841 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 DB 841 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 QY 901 AAGCAAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
 DB 901 AAGCAAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
 QY 961 GCTTTCTTCACGTTGTCTGAAACCCCATCTGATCTCTTCTGAGGCAAAATTTAAA 1020
 DB 961 GCTTTCTTCACGTTGTCTGAAACCCCATCTGATCTCTTCTGAGGCAAAATTTAAA 1020
 QY 1021 ACCTTGCCGAGAGGAGTCACTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
 DB 1021 ACCTTGCCGAGAGGAGTCACTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
 QY 1081 AAGGAAAGGAGGAGTCACTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
 DB 1081 AAGGAAAGGAGGAGTCACTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
 QY 1141 TCCAGCTAACAGAGTCACTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
 DB 1141 TCCAGCTAACAGAGTCACTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
 QY 1201 ACACATTTTTCAGATATATAAGAGTCACTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGG 1260
 DB 1201 ACACATTTTTCAGATATATAAGAGTCACTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGG 1260

QY 1261 TTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 DB 1261 TTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 QY 1321 TTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
 DB 1321 TTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
 QY 1381 GTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
 DB 1381 GTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
 QY 1441 TAAAGCTAGAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
 DB 1441 TAAAGCTAGAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
 QY 1501 GTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 DB 1501 GTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 QY 1561 AAGTGTATAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
 DB 1561 AAGTGTATAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
 QY 1621 AGTGTACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
 DB 1621 AGTGTACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
 QY 1681 AA 1737
 DB 1681 AA 1737

RESULT 3
 Q29506
 ID Q29506 standard; DNA: 1737 BP.
 AC Q29506;
 DT 12-MAR-1993 (first entry)
 DE New platelet factor 4 receptor superfamily member PF4AR1.
 KW IL-8R; G-protein coupled receptor family; rhodopsin superfamily;
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT 91..1149
 FT cds
 PN M09217497-A.
 PD 15-OCT-1992.
 PF 23-MAR-1992: U02317.
 PR 29-MAR-1991: US-677211.
 PR 19-DEC-1991: US-810782.
 PA (GETH) GENENTECH INC.
 PI Holmes WE, Lee J, Wood WI:
 DR WPI: 92-366191/74.
 DR P-PSDB: R27792.
 PT Isolated human platelet factor 4 super-family receptor
 PT polypeptide and corresp. antibodies and DNA - useful as
 PT diagnostic and screening agents, and for treating inflammation or
 PT PF4AR-mediated disorders
 CC Claim 7; Fig 4; 78pp; English.
 CC The IL-8 receptor cDNA sequence was isolated (see Q29505) and a
 CC 874bp sub-fragment of the coding sequence was used as a probe to
 CC screen human cell line Hu60 and human peripheral blood lymphocyte
 CC cDNA libraries. Two new gene sequences were found that are clearly
 CC related to the IL-8 receptor. One of these was contained in
 CC combined clone 8rr-20.15 and is predicted to encode an amino acid
 CC sequence which is 34% identical with both the high and low affinity
 CC IL-8 receptors. See also Q37107.
 SO Sequence 1737 BP; 457 A; 412 C; 370 G; 498 T;

Query Match 99.6%; Score 1730.6; DB 1; Length 1737;
 Best Local Similarity 99.8%; Pred. No. 0;

Matches 1733; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1 GAATTCATGTGCTGGCGGCGGCGCAAGTACGCGGAGGCGCTGAGTCTCCAGTA 60
Db 1 GAATTCATGTGCTGGCGGCGGCGCAAGTACGCGGAGGCGCTGAGTCTCCAGTA 60
QY 61 GCCACCGCATCTGAGAACACGAGGCTTACCATGAGGGGATCATATATACACTTCAGAT 120
Db 61 GCCACCGCATCTGAGAACACGAGGCTTACCATGAGGGGATCATATATACACTTCAGAT 120
QY 62 GCCACCGCATCTGAGAACACGAGGCTTACCATGAGGGGATCATATATACACTTCAGAT 120
Db 62 GCCACCGCATCTGAGAACACGAGGCTTACCATGAGGGGATCATATATACACTTCAGAT 120
QY 121 AACTACACCGAGAAATGGGCTCAGGGAGTATGACTCCATGAGGAACCTGTTCCGT 180
Db 121 AACTACACCGAGAAATGGGCTCAGGGAGTATGACTCCATGAGGAACCTGTTCCGT 180
QY 122 AACTACACCGAGAAATGGGCTCAGGGAGTATGACTCCATGAGGAACCTGTTCCGT 180
Db 122 AACTACACCGAGAAATGGGCTCAGGGAGTATGACTCCATGAGGAACCTGTTCCGT 180
QY 181 GAAGAATAATGCTATTTCAATAAATCTTCGCGGACCATGACATCCATCTCTTA 240
Db 181 GAAGAATAATGCTATTTCAATAAATCTTCGCGGACCATGACATCCATCTCTTA 240
QY 241 ACTGCGATTGTGGCAATGATGATCATCTGTCATGGGTTACGAGAAACTGAGA 300
Db 241 ACTGCGATTGTGGCAATGATGATCATCTGTCATGGGTTACGAGAAACTGAGA 300
QY 301 AGCATGACGAGACAGTACAGGCTGACCTGTAGTGGCCGACCTCTTTGTATCAGC 360
Db 301 AGCATGACGAGACAGTACAGGCTGACCTGTAGTGGCCGACCTCTTTGTATCAGC 360
QY 361 CTTCCTCTTGGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 361 CTTCCTCTTGGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 GGAGTCATGTCATCTACACAGTCAACCTCTACAGGAGTGTCTCATCTGCGCTTCATC 480
Db 421 GGAGTCATGTCATCTACACAGTCAACCTCTACAGGAGTGTCTCATCTGCGCTTCATC 480
QY 481 AGTCTGACCGCTACTGCTGCGCATGCTCCACGCCACCAAGTACAGAGCCCAAGAGCTG 540
Db 481 AGTCTGACCGCTACTGCTGCGCATGCTCCACGCCACCAAGTACAGAGCCCAAGAGCTG 540
QY 541 TTGGCTGAAAGGTGGTGTATGTTGGGCTGTGGATCCGCGCTCTGCTGATATCC 600
Db 541 TTGGCTGAAAGGTGGTGTATGTTGGGCTGTGGATCCGCGCTCTGCTGATATCC 600
QY 601 GACTTCATCTTTCACACGTCAGTACGAGGAGATGACAGATATATCTGTGACGCTTCTAC 660
Db 601 GACTTCATCTTTCACACGTCAGTACGAGGAGATGACAGATATATCTGTGACGCTTCTAC 660
QY 661 CCCAATGACTTGTGGGTGTGTTGTTCCAGTTTCACACATCATGTTGGCTTATCTG 720
Db 661 CCCAATGACTTGTGGGTGTGTTGTTCCAGTTTCACACATCATGTTGGCTTATCTG 720
QY 721 CCGGTAATGTATCTGTCGCTGCTATGTCATATCATCTCCAAAGTGCACACCTCCAG 780
Db 721 CCGGTAATGTATCTGTCGCTGCTATGTCATATCATCTCCAAAGTGCACACCTCCAG 780
QY 781 GGGCACCAGAAAGGCGAAGCCCTCAAGACACAGTATCTCTGCTTCTTCTGCGC 840
Db 781 GGGCACCAGAAAGGCGAAGCCCTCAAGACACAGTATCTCTGCTTCTTCTGCGC 840
QY 841 TGTGGCTGCTTACTACATTTGGGATCAGATGACTCTTCTTCTCTGGAATCATC 900
Db 841 TGTGGCTGCTTACTACATTTGGGATCAGATGACTCTTCTTCTCTGGAATCATC 900
QY 901 AAGCAAGGATGATGATTTGAGAACATGTCACATGATGATTCATCCAGGCGCTTA 960
Db 901 AAGCAAGGATGATGATTTGAGAACATGTCACATGATGATTCATCCAGGCGCTTA 960
QY 961 GCTTCTTCTACATGTTGTGAAACCCCATCTCTATGCTTCTTCTGAGCAAAATTTAA 1020
Db 961 GCTTCTTCTACATGTTGTGAAACCCCATCTCTATGCTTCTTCTGAGCAAAATTTAA 1020
QY 1021 ACCTCTGCGCAGCAGCAGTACCTCTGTGAGAGAGGGTCCAGCTCAAGATCTCTCC 1080
Db 1021 ACCTCTGCGCAGCAGCAGTACCTCTGTGAGAGAGGGTCCAGCTCAAGATCTCTCC 1080

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QY 1081 AAAGGAAGCGAGGTGAGCATTCATCTGTTCCACTGAGTCCAGTCAAGTTTTCAC 1140
Db 1081 AAAGGAAGCGAGGTGAGCATTCATCTGTTCCACTGAGTCCAGTCAAGTTTTCAC 1140
QY 1141 TCCAGCTAACACAGATGTAAAGACTTTTATATAGATTAATTAAGTTTAAAGTT 1200
Db 1141 TCCAGCTAACACAGATGTAAAGACTTTTATATAGATTAATTAAGTTTAAAGTT 1200
QY 1201 ACACATTTTACAGATATTAAGACTGACCAATATTGACAGTTTTATGCTTTGAT 1260
Db 1201 ACACATTTTACAGATATTAAGACTGACCAATATTGACAGTTTTATGCTTTGAT 1260
QY 1261 TTTGCTGCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1320
Db 1261 TTTGCTGCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1320
QY 1321 TTTGCTGCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1380
Db 1321 TTTGCTGCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1380
QY 1381 GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
Db 1381 GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1441 TAAAGCTGAATATGATCCCGAGCTGTTATGATGATTAATCTCCATTCGCTGAGAC 1500
Db 1441 TAAAGCTGAATATGATCCCGAGCTGTTATGATGATTAATCTCCATTCGCTGAGAC 1500
QY 1501 GTTTTCTGCTGCTTAAAGCTGATTTTCTGTAGAGATGAGCACTTAACCAAGCCC 1560
Db 1501 GTTTTCTGCTGCTTAAAGCTGATTTTCTGTAGAGATGAGCACTTAACCAAGCCC 1560
QY 1561 AAAGTGTATGAAATGCTGTTTCAAGTTTCAAGTGTGGTGTATTCAGCACTTAC 1620
Db 1561 AAAGTGTATGAAATGCTGTTTCAAGTTTCAAGTGTGGTGTATTCAGCACTTAC 1620
QY 1621 AGTGTACAGTCTGTTATTAAGTTTAAATTAAGTATTAAGTTTAAATTAAGTTT 1680
Db 1621 AGTGTACAGTCTGTTATTAAGTTTAAATTAAGTATTAAGTTTAAATTAAGTTT 1680
QY 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1737
Db 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1737

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RESULT 4

X15882 standard; cDNA; 1944 BP.

AC X15882:

DE 12-MAY-1999 (first entry)

DE cDNA encoding G-protein coupled receptor polypeptide designated CXCR4B.

KM G-protein coupled receptor; CXCR4B; human; splice variant;

KM chemokine receptor; CXCR4; vaccine; gene therapy; HIV-1; HIV-1;

KM cancer; pain; diabetes; obesity; anorexia; bulimia; asthma;

KM Parkinson's disease; acute heart failure; hypotension; hypertension;

KM urinary retention; osteoporosis; angina pectoris; myocardial infarction;

KM stroke; ulcer; allergy; benign prostatic hypertrophy; migraine;

KM vomiting; psychotic disorder; neurological disorder; anxiety;

KM schizophrenia; manic depression; delirium; dementia; mental retardation;

KM dyskinesias; Huntingtons disease; Gilles de la Tourette syndrome; ss.

OS Homo sapiens.

FN Key

FN CDS location/qualifiers

FN 336..1406

FN /*tag- a

FN misc-feature 361

FN /*tag- b

FN /*note- "splice acceptor site"

EP-897980-A2.

PD 24-FEB-1999.

PD 07-AUG-1998; 306324.

PR 24-JUL-1998; US-056601.

PR 20-AUG-1997; US-056601.

PA (SMIX) SMITHKLINE BEECHAM CORP.
PI Gupta SK, Pillariseti K;
DR WPI: 99-134643/12.
PR P-PSDB: W97362.
PT New G protein coupled receptor (CXCR4B) polypeptide and
PT polynucleotide, human splice variant of a chemokine receptor -
PT useful as diagnostic reagents and for prevention and treatment of
PT HIV infection, cancer, stroke and dementia
PS Claim 2: Page 16-17; 24pp; English.
CC The present sequence encodes a G-protein coupled receptor polypeptide
CC designated CXCR4B, which is a human splice variant of a chemokine
CC receptor CXCR4. CXCR4B polynucleotides and polypeptides are useful for
CC diagnosing susceptibility to diseases by detecting mutations or
CC polymorphisms in the CXCR4B gene or analysing for the presence or amount
CC of CXCR4B polypeptide expressed in a patient. CXCR4B polypeptides and
CC polynucleotides are also useful for screening for antagonists and
CC agonists which can be used to treat conditions associated with CXCR4B
CC polypeptide imbalance. CXCR4B polypeptides can be administered directly
CC (as a vaccine) or via a vector (gene therapy) to prevent disease.
CC Diseases diagnosed, prevented and treated include: HIV-1 and HIV-1
CC infections; cancer; pain; diabetes; obesity; anorexia; bulimia; asthma;
CC Parkinson's disease; acute heart failure; hypotension; hypertension;
CC urinary retention; osteoporosis; angina pectoris; myocardial infarction;
CC stroke; ulcers; allergies; benign prostatic hypertrophy; migraine;
CC vomiting; psychotic and neurological disorders, including anxiety,
CC schizophrenia, manic depression, delirium, dementia and severe mental
CC retardation; and dyskinesias, such as Huntington's disease or Gilles de
CC la Tourette syndrome. CXCR4B polypeptides are useful for mapping genes
CC to chromosomes, allowing gene inheritance to be studied through linkage
CC analysis.
SQ Sequence 1944 BP; 497 A; 437 C; 412 G; 596 T;

Query Match 90.3%; Score 1569.2; DB 1; Length 1944;
Best Local Similarity 99.8%; Pred. No. 3e-282;
Matches 1579; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

OY 106 ATATCACTTCGATACACACGAGAAATGGGCTCGGGGACATACATCCATGAAG 165
DB 363 ATATCACTTCGATACACACGAGAAATGGGCTCGGGGACATACATCCATGAAG 422
OY 166 GAACCCCTGTCGTAAGAAAAATGCTAATTTCAATAAATCTTCTGCCACCATCTAC 225
DB 423 GAACCCCTGTCGTAAGAAAAATGCTAATTTCAATAAATCTTCTGCCACCATCTAC 482
OY 226 TCCATCATCTTTTAACTGACATTGTGGCAATGGATTGCTATCCTGGTCAATGGTTAC 285
DB 483 TCCATCATCTTTTAACTGACATTGTGGCAATGGATTGCTATCCTGGTCAATGGTTAC 542
OY 286 CAGAAGAACTGAGAGACTGACGGACAGTACAGGCTGCACCTGATGCGCCAGACCTC 345
DB 543 CAGAAGAACTGAGAGACTGACGGACAGTACAGGCTGCACCTGATGCGCCAGACCTC 602
OY 346 CTCCTTGTATCAGCCTTCCCTTCTGGGAGTTGATGCCGTGGCAAACTGTACTTTGGG 405
DB 603 CTCCTTGTATCAGCCTTCCCTTCTGGGAGTTGATGCCGTGGCAAACTGTACTTTGGG 662
OY 406 AACTTCCATGGAAGGAGCTGCTATGCTACATCTACAGTCAACCTCTACAGCAGTGTCTC 465
DB 663 AACTTCCATGGAAGGAGCTGCTATGCTACATCTACAGTCAACCTCTACAGCAGTGTCTC 722
OY 466 ATCCGTGGCTTCATCAGTCTGAGCGCTACCTGCGCATGCTCAGCGCCCAACAGTGA 525
DB 723 ATCCGTGGCTTCATCAGTCTGAGCGCTACCTGCGCATGCTCAGCGCCCAACAGTGA 782
OY 526 AGGCCAAGAACCTGTGGCTGAAAAAGTGTCTATGTTGGGCTGTGATCCCTGCCCTC 585
DB 783 AGGCCAAGAACCTGTGGCTGAAAAAGTGTCTATGTTGGGCTGTGATCCCTGCCCTC 842
OY 586 CTGCTGACTATTCCGAGACTCATCTTTGGCAAGCTCAGTGAAGGAGATGACAGATATATC 645
DB 843 CTGCTGACTATTCCGAGACTCATCTTTGGCAAGCTCAGTGAAGGAGATGACAGATATATC 902

OY 646 TGTGACCCGCTTATACCCAAATGACTTTGGGGTGTGTTGTTCCAGTTCCAGCATATG 705
DB 903 TGTGACCCGCTTATACCCAAATGACTTTGGGGTGTGTTGTTCCAGTTCCAGCATATG 962
OY 706 GTTGGCTTATCCGCTGCTGTTGTCATCCGCTCCTCATATGATATATATCTCCAG 765
DB 963 GTTGGCTTATCCGCTGCTGTTGTCATCCGCTCCTCATATGATATATATCTCCAG 1022
OY 766 CTGTACACATCCAAAGGCGCCACAGAGGCAAGGCGCTCAAGACCAAGTCACTCCATC 825
DB 1023 CTGTACACATCCAAAGGCGCCACAGAGGCAAGGCGCTCAAGACCAAGTCACTCCATC 1082
OY 826 CTGGCTTTCTTGCTGCTGTTGGCTGCTTACTACATTTGAGATCAGATGACTCTTATC 885
DB 1083 CTGGCTTTCTTGCTGCTGTTGGCTGCTTACTACATTTGAGATCAGATGACTCTTATC 1142
OY 886 CTCCTGGAAATATACAGAGGAGTGTAGTTTGAACACGTGTCACAGTGGATTC 945
DB 1143 CTCCTGGAAATATACAGAGGAGTGTAGTTTGAACACGTGTCACAGTGGATTC 1202
OY 946 ATACCCGAGGCGCTTACTTCTTCCACTGTTGTCTGAACCCCATCCTATGCTTCTCT 1005
DB 1203 ATACCCGAGGCGCTTACTTCTTCCACTGTTGTCTGAACCCCATCCTATGCTTCTCT 1262
OY 1006 GGAGCCAAATTTAAACCTCTGCCCAGCAGCAGTCACTCCTCTGTGACAGAGGCTCCAGC 1065
DB 1263 GGAGCCAAATTTAAACCTCTGCCCAGCAGCAGTCACTCCTCTGTGACAGAGGCTCCAGC 1322
OY 1066 CTCAGATCTCTCCAAAGAAAGGAGGTGACATCTATGTTCCACAGTACTAG 1125
DB 1323 CTCAGATCTCTCCAAAGAAAGGAGGTGACATCTATGTTCCACAGTACTAG 1382
OY 1126 TCTTCAAGTTTCACTCGAGCTAACACAGATGTAAAGACTTTTATATACGATATA 1185
DB 1383 TCTTCAAGTTTCACTCGAGCTAACACAGATGTAAAGACTTTTATATACGATATA 1442
OY 1186 ACTTTTATTAAGTATACATTTTTCATATATAAAGCTGACCAATATTGACAGTTT 1245
DB 1443 ACTTTTATTAAGTATACATTTTTCATATATAAAGCTGACCAATATTGACAGTTT 1502
OY 1246 TATTCCTGTTGGATTTTGTCTGTTCTTCTTGAATTTTGTGAAGTTAATTACTTA 1305
DB 1503 TATTCCTGTTGGATTTTGTCTGTTCTTCTTGAATTTTGTGAAGTTAATTACTTA 1562
OY 1306 TTTATATATAATTTTGTGTTTCATATGATGTGTCTAGGACAGACTGTGCCAAGT 1365
DB 1563 TTTATATATAATTTTGTGTTTCATATGATGTGTCTAGGACAGACTGTGCCAAGT 1622
OY 1366 TCTTAGTGTGATGCTGCTGCTGAGAGACTGTAAAGGAAGTGAACATTCAGAGC 1425
DB 1623 TCTTAGTGTGATGCTGCTGCTGAGAGACTGTAAAGGAAGTGAACATTCAGAGC 1682
OY 1426 GTTAGTAATCAGCTAAGCTAGAAATGATCCAGCTGTTATGCAATATATCTCT 1485
DB 1683 GTTAGTAATCAGCTAAGCTAGAAATGATCCAGCTGTTATGCAATATATCTCT 1742
OY 1486 CCATTCGCCGTGGAAGCTTTTCTCTGTTTAAAGACGTATTTTGTGTGAAGATGAC 1545
DB 1743 CCATTCGCCGTGGAAGCTTTTCTCTGTTTAAAGACGTATTTTGTGTGAAGATGAC 1802
OY 1546 TTATATACCAAGCCCAAGTGTATGAAATGCTGTTTCAAGTTTCAGAGTGGGT 1605
DB 1803 TTATATACCAAGCCCAAGTGTATGAAATGCTGTTTCAAGTTTCAGAGTGGGT 1862
OY 1606 GATTTACAGCTTACAGTGTAC - AGCTTGTATTAAGTTGTTAAATGAATGATGTTAA 1664
DB 1863 GATTTACAGCTTACAGTGTACAGTGTGATTAAGTTGTTAAATGAATGATGTTAA 1922
OY 1665 ACTTAAAAAATTTTAAAAAATTTTAAAAA 1686
DB 1923 ACTTAAAAAATTTTAAAAAATTTTAAAAA 1944

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RESULT 5
ID V18357 standard; DNA: 1317 BP.
AC V18357;
DE 25-SEP-1998 (first entry)
KW Human RM3 seven transmembrane (7TM) receptor cDNA..
KW V28; Placenta; seven transmembrane receptor; 7TM; signal transduction;
OS Immunology; inflammation; RM3; SS.
FH Homo sapiens.
FT key Location/Qualifiers
FT CDS 201..1211
FT /lag= a
FT /product= "Human RM3 seven transmembrane receptor"
PD US5759804-A.
PD 02-JUN-1998.
PD 17-NOV-1993; 153848.
PR 17-NOV-1992; US-977452.
PA (ICOS-) ICOS CORP.
PI Godiska R, Gray PW, Schweickart VL;
PI MPI; 98-332132/29.
DR P-PSDB: W48734.
PT DNA encoding V28 seven transmembrane receptor polypeptide - useful
PT for producing recombinant polypeptide and anti-V28 antibodies, and
PT in screening assays for V28 agonists and antagonists
PS Example 11; Columns 89-94; 56bp; English.
CC The present novel sequence represents the human RM3 cDNA, isolated
CC from a human macrophage cDNA library. The invention claims for
CC the full length V28 genomic DNA sequence (V18343) isolated from a human
CC placenta genomic library. The V28 (W48722) and RM3 proteins are seven
CC transmembrane (7TM) receptors which are probably involved in signal
CC transduction. The invention also claims that cells transformed with
CC V28 DNA can be used to produce the recombinant polypeptide, to produce
CC anti-V28 antibodies or in screening assays for V28 agonists or
CC antagonists. The antibodies, agonists and antagonists could then be
CC used to modulate V28 receptor-ligand binding, for e.g. in immunological
CC and/or inflammatory events in vivo.
SQ Sequence 1317 BP; 332 A; 342 C; 265 G; 378 T;

Query Match 64.4%; Score 1118.2; DB 1; Length 1317;
Best Local Similarity 99.6%; Pred. No. 8,4e-199;
Matches 1131; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 106 ATATACATTAGATTAACACCGAGGAATGGGCTCAGGGAGTATGATCCATGAG 165
DB 171 ATATACATTAGATTAACACCGAGGAATGGGCTCAGGGAGTATGATCCATGAG 230
QY 166 GAACCCGTTCCGTCGAAGAAATGCTAATTCAATAAATCTTCCTGCCACATCTAC 225
DB 231 GAACCCGTTCCGTCGAAGAAATGCTAATTCAATAAATCTTCCTGCCACATCTAC 290
QY 226 TCCATCATCTTTAACTGATGCGCATTTGGGCAATGGATGTCATCTCGTCAGTGGTAC 285
DB 291 TCCATCATCTTTAACTGATGCGCATTTGGGCAATGGATGTCATCTCGTCAGTGGTAC 350
QY 286 CAGAGAAGAACTGAGAGCATGACGAGCAAGTACAGGCTGCACCTGCTCAAGTGGCGACCTC 345
DB 351 CAGAGAAGAACTGAGAGCATGACGAGCAAGTACAGGCTGCACCTGCTCAAGTGGCGACCTC 410
QY 346 CTCTTTGTCATCAGGCTTCCTCTTGGGAGTTGATGCCGTGGCAAACTGGTACTTTGGG 405
DB 411 CTCTTTGTCATCAGGCTTCCTCTTGGGAGTTGATGCCGTGGCAAACTGGTACTTTGGG 470
QY 406 AACTTCCTATGCAAGGAGCTGCATGTCATCTACAGTCAAGTCAACTGACAGAGTGGCTTC 465
DB 471 AACTTCCTATGCAAGGAGCTGCATGTCATCTACAGTCAAGTCAACTGACAGAGTGGCTTC 530
QY 466 ATCTTGCCCTTATCATGCTGTCAGCCGCTACCTGGCCATGCTCCAGCCCAACAGTGCAG 525
DB 531 ATCTTGCCCTTATCATGCTGTCAGCCGCTACCTGGCCATGCTCCAGCCCAACAGTGCAG 590
QY 526 AGGCCAAGGAAGCTGTGGCTGAAGAGTGCTATGTTGGGCTGTGGATCCCTGCTC 585
DB 585 AGGCCAAGGAAGCTGTGGCTGAAGAGTGCTATGTTGGGCTGTGGATCCCTGCTC 650
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DB 591 AGGCCAAGGAAGCTGTGGCTGAAGAGTGCTATGTTGGGCTGTGGATCCCTGCTC 650
QY 586 CTGCTGACTATTTCCGAGCACTTCTTTGGCAACGTCAGTGGAGGAGATGACAGATATTC 645
DB 651 CTGCTGACTATTTCCGAGCACTTCTTTGGCAACGTCAGTGGAGGAGATGACAGATATTC 710
QY 646 TGTGACCGCTTACCCCAATGACTTGGGGTGTGGTGTGTTCCAGTTCAGACATCATG 705
DB 711 TGTGACCGCTTACCCCAATGACTTGGGGTGTGGTGTGTTCCAGTTCAGACATCATG 770
QY 706 GTTGGCCCTTATCTGCTGGTGTATTTGTCATCTGCTCTGCTATGATATATCTCCAG 765
DB 771 GTTGGCCCTTATCTGCTGGTGTATTTGTCATCTGCTCTGCTATGATATATCTCCAG 830
QY 766 CTGTCACTCACTCAAGGAGCCACAGAGGCAAGGCCCTCAAGACCACAGTATCTCTC 825
DB 831 CTGTCACTCACTCAAGGAGCCACAGAGGCAAGGCCCTCAAGACCACAGTATCTCTC 890
QY 826 CTGGCTTTCTTGCTGCTGTGGCTGCTTACTACATTTGGATCAGCATGACTCTTCATC 885
DB 891 CTGGCTTTCTTGCTGCTGTGGCTGCTTACTACATTTGGATCAGCATGACTCTTCATC 950
QY 886 CTCTGGAATATCATAGCAAGGAGTGTAGTTGAGAACACTGTGCACAAATGATTTCC 945
DB 951 CTCTGGAATATCATAGCAAGGAGTGTAGTTGAGAACACTGTGCACAAATGATTTCC 1010
QY 946 ATACCCGAGGCGCTAGCTTTCTTCACATGTTGTGTCGAACCCATCTCTATCTTCTT 1005
DB 1011 ATACCCGAGGCGCTAGCTTTCTTCACATGTTGTGTCGAACCCATCTCTATGCTTTCTT 1070
QY 1006 GGAGCCAAATTTAAACTCTGCGCCAGCAGCAGTCTGCTGTGAGCAGAGGCTCCAGC 1065
DB 1071 GGAGCCAAATTTAAACTCTGCGCCAGCAGCAGTCTGCTGTGAGCAGAGGCTCCAGC 1130
QY 1066 CTCAGATCTCTCTCAAGAAAGAGGAGTGGACATTCATGTTCCACAGTCTGAG 1125
DB 1131 CTCAGATCTCTCTCAAGAAAGAGGAGTGGACATTCATGTTCCACAGTCTGAG 1190
QY 1126 TCTTCAAGTTTCACTCAGCTTAACACAGATGTAAAGACTTTTATACGATAATA 1185
DB 1191 TCTTCAAGTTTCACTCAGCTTAACACAGATGTAAAGACTTTTATACGATAATA 1249
QY 1186 ACTTTTATAGTATACATTTTTCAGATATTAAGACAGTCAATATTTGTACA 1240
DB 1250 ACTTTTATAGTATACATTTTTCAGATATTAAGACAGTCAATATTTGTAAA 1304

RESULT 6
ID 066179 standard; cDNA: 1317 BP.
AC 066179;
DE 07-FEB-1995 (first entry)
DE Seven transmembrane receptor (RM3) coding sequence.
KW Primer; seven transmembrane receptor; receptor; amplification; PCR;
OS Polymerase chain reaction; ss.
FH Homo sapiens.
FT key Location/Qualifiers
FT CDS 201..1214
FT /lag= a
FT /product= "Seven transmembrane receptor"
PD M09412635-A.
PD 09-JUN-1994.
PD 17-NOV-1993; U11153.
PR 17-NOV-1992; US-977452.
PA (ICOS-) ICOS CORP.
PI Godiska R, Gray PW, Schweickart VL;
PI MPI; 94-200264/24.
DR P-PSDB: R53753.
PT DNA encoding seven transmembrane receptors - used to develop
PT prods. for use as therapeutic or diagnostic agents for conditions
PT involving the receptors.
PS Example 11; Page 82-83; 100bp; English.
Two primers (066148, 066149) were used in a PCR reaction containing
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CC human macrophage cDNA library in plasmid pRC/CMV. When the PCR products were subjected to agarose gel electrophoresis a faint band of 180-200 base pairs was observed. Re-amplified material was digested with BamHI and HindIII and cloned into the plasmid Bluescript SK-. Of sixteen clones sequenced, two contained a unique CC sequence termed RM3. Specific primers for the partial RM3 clone were used to identify this full length RM3 cDNA clone.

Query Match 64.3%; Score 1116.6; DB 1; Length 1317;
Best Local Similarity 99.6%; Pred. No. 1.7e-198;
Matches 1130; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

CC 106 ATATACCTTACAGTACATACACCGAAGTGGCTCAGGGGAGTATGACTCCATGAAG 165
CC 171 ATATACACTTACAGTACATACACCGAAGTGGCTCAGGGGAGTATGACTCCATGAAG 230
CC 166 GAACCCCTGTTCCGTCAGAAATGCTAATTTCAATAAATCTCCGCCACCATCTAC 225
CC 231 GAACCCCTGTTCCGTCAGAAATGCTAATTTCAATAAATCTCCGCCACCATCTAC 290
CC 226 TCCATCATCTTCTTAACTGCGATGTCGCAATGATGTCATCTGTCATGCTTAC 285
CC 291 TCCATCATCTTCTTAACTGCGATGTCGCAATGATGTCATCTGTCATGCTTAC 350
CC 286 CAGAGAAATGAGAGCATGAGGAGCAATGACGCTGCACCTGTCAGTGGCCGACCTC 345
CC 351 CAGAGAAATGAGAGCATGAGGAGCAATGACGCTGCACCTGTCAGTGGCCGACCTC 410
CC 346 CTCTTGTGTCACAGGCTTCCCTTGGGAGTTGATGCGGCGAACTGGTACTTTGGG 405
CC 411 CTCTTGTGTCACAGGCTTCCCTTGGGAGTTGATGCGGCGAACTGGTACTTTGGG 470
CC 406 AACTTCTATGACAGGAGTCATGTCATCTACACAGTCAACCTCTACAGAGTGTCTC 465
CC 471 AACTTCTATGACAGGAGTCATGTCATCTACACAGTCAACCTCTACAGAGTGTCTC 530
CC 466 ATCTGCGCTTTCATCACTGTCGACCGTACTGCGCATGTCACAGGCGACCAACAGTCAG 525
CC 531 ATCTGCGCTTTCATCACTGTCGACCGTACTGCGCATGTCACAGGCGACCAACAGTCAG 590
CC 526 AGGCAAGAGAGTGTGGCTGAAAGAGTGTGATGTTGGCGCTGATCCCGGCTC 585
CC 591 AGGCAAGAGAGTGTGGCTGAAAGAGTGTGATGTTGGCGCTGATCCCGGCTC 650
CC 586 CTGCTGACTATTCGCGACTTATCTTTCGCAAGCTCAGTGAAGGAGATGACATATATC 645
CC 651 CTGCTGACTATTCGCGACTTATCTTTCGCAAGCTCAGTGAAGGAGATGACATATATC 710
CC 646 TGTGACCGCTTACCCCATGACTTGTGGTGTGTGTTCAGTTTCAGACATCATG 705
CC 711 TGTGACCGCTTACCCCATGACTTGTGGTGTGTGTTCAGTTTCAGACATCATG 770
CC 706 GTTGGCTTATCTGCTGATGATGTCATCTGCTGATGATGATGATGATGATGATG 765
CC 771 GTTGGCTTATCTGCTGATGATGTCATCTGCTGATGATGATGATGATGATGATG 830
CC 766 CTGCTGACTTCAAGGAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 825
CC 831 CTGCTGACTTCAAGGAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 890
CC 826 CTGCTGACTTCAAGGAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 885
CC 891 CTGCTGACTTCAAGGAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 950
CC 886 CTGCTGAAATTCATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 945
CC 951 CTGCTGAAATTCATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1010
CC 946 ATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1005
CC 1011 ATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1070

CC 1006 GAGCCAAATTTAAACCTCTGCCACAGCAGCAGTCACTCTGTGAGCAGAGGGTCCAGC 1065
CC 1071 GAGCCAAATTTAAACCTCTGCCACAGCAGCAGTCACTCTGTGAGCAGAGGGTCCAGC 1130
CC 1066 CTCAAGATCTCTCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1125
CC 1131 CTCAAGATCTCTCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1190
CC 1126 TCTCAAGTTTCACTGACCTCAACAGATGTAAGACTTTTTCATGATTAATA 1185
CC 1191 TCTCAAGTTTCACTGACCTCAACAGATGTAAGACTTTTTCATGATTAATA 1249
CC 1186 ACTTTTTTAACTTACATTTTTCAGATATAAAGACTGACCAATATTGTACA 1240
CC 1250 ACTTTTTTAACTTACATTTTTCAGATATAAAGACTGACCAATATTGTAAAA 1304

RESULT 7

V46370
ID V46370 standard; cDNA to mRNA; 1877 BP.
AC V46370;
DT 20-NOV-1998 (first entry)
DE Nucleic acid encoding a murine CXCR chemokine receptor.
KW Mouse; CXCR chemokine receptor; pre-B cell line DM34;
KW CXCR chemokine pre-B cell stimulatory factor PBSF/SDF-1;
OS HIV infection; screening; inhibitor; AIDS; ds.
MS Mus sp.
FH Key
FT Location/Qualifiers
FT 120..1199
FT CDS
PN W09835035-A1.
PD 13-AUG-1998.
PE 07-FEB-1997; J00299.
PR 07-FEB-1997; W0-J00299.
PA (SHIO.) SHIONOGI & CO LTD.
PI Iizasa H, Kishimoto T, Nagasawa T, Nakajima T, Tachibana K,
PI Yoshida N, Yoshie O;
DR WPI: 98-447232/38.
DR P-PSDB: W64778.
PT Mouse CXCR chemokine receptor binding to PBSF/SDF-1 pre-B cell
PT stimulatory factor - is useful for screening of potential HIV
PT infection and AIDS inhibitors
PS Claim 3; Pages 39-42; 76pp; Japanese.
CC The present sequence encodes a murine CXCR chemokine receptor which
CC binds to the mouse CXCR chemokine pre-B cell stimulatory factor
CC PBSF/SDF-1. The nucleic acid is isolated from mouse pre-B cell
CC line DM34. The receptor and cells expressing it can be used in the
CC study and mapping of the mechanism of HIV infection and in screening
CC of potential inhibitors of HIV infection and the development of AIDS.
CC Sequence 1877 BP; 469 A; 451 C; 406 G; 551 T;

Query Match 56.1%; Score 974.4; DB 1; Length 1877;
Best Local Similarity 76.1%; Pred. No. 3.7e-172;
Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;

CC 20 GCGGCGGCGAAGTGAAGCGCGGCTGAGTCTCCAGTAGCCACCGCATCTGAGAAC 79
CC 50 GCAGGTAGCAGTAGTACCTCTGAGGCGCTTGTGCTCCGTAACACACGAGCTGAGAGC 109
CC 80 CAGCGGTACCATGGA-----GGGATCAGTATATACCTTCAATATACACCGAGGA 134
CC 110 GAGTGTGCGATGGAACCGATGAGTGAATATATACCTTCAATATACCTGTAAGA 169
CC 135 AATGGCTCAGGAGTATGATCTCATGAAGAACCTGTTTCCGTAAGAAATGCTAA 194
CC 170 AGTGGGTGTGAGATATGATCTCAACAAAGAACCTGTTTCCGTAAGAAATGCTAA 229
CC 195 TTTCATTAATTTCTCTGCGCACCATCTAGTCCATCATCTTTTAACGTGATGAGG 254
CC 230 TTTCATTAATTTCTCTGCGCACCATCTAGTCCATCATCTTTTAACGTGATGAGG 289

OY	255	CAATGATGGTCAATCTGTGTCATGGTTACCGAAGAAACCTGAGAAAGCATACGGACAA	314
Db	290	CAATGGAATGGTGAACCTGTGGTCATGGGATTACCGAAGAAAGCATAAAGAGCATACGGACAA	349
OY	315	GTACAGGCTGACCTGTGCAGTGGGCGGACCTCCTTTGATCAGACCTTCCTTCGGGC	374
Db	350	GTACCGGCTGCACCTGTGCAGTGGCTGACCTCCTTTGATCAGACCTTCCTTCGGGC	409
OY	375	AGTTGATGCCGTGGCAAACTGGTACTTTGGGAATTCCTATGCAAGGCAAGTCATGTCAAT	434
Db	410	AGTTGATGCCATGGCTGACCTGAGTGTACTTTGGGAATTTTGTGTAAGGCTGTCCATATCAT	469
OY	435	CTACACAGTCAACCTCTACAGCAGATGTCCATATCCGTGGCTTCATATAGCTGGACCGCTA	494
Db	470	CTACACTGTCAACCTCTACAGCAGACCGTTCTCATATCCGTGGCTTCATATAGCTGGACCGGA	529
OY	495	CCTGGCCATCTCTCCAGCCGCAACCAAGATCTCAGAGGGCCAAAGGAAGCTTGGGTGAAGAAAGT	554
Db	530	CCTGGCCATTGTCCAGCCGCAACCAAGATCTCAGAGGGCCAAAGGAAGCTTGGGTGAAGAAAGC	589
OY	555	GGTCTATGTTGGCGTCTGGATCCCTGGCCCTCCTGTGACTATATCCGAGTTCATCTTTGC	614
Db	590	AGTCAATGTGGCGTCTGGATCCAGCCCTCCTGTGACTATATCCTGATTCATCTTTGC	649
OY	615	CACG-----TCAATGAGCGAGATGACAGTAATATGTGACCCGCTCTCA	659
Db	650	CGAGCTCAGCCAGGGGGGACATCACTACGTGGGGGATGACAGGTATCATGTGGACCGCTTTA	709
OY	660	CCCCATGACTTTGGGGGTGTGTGTCCAGTTTCAGACATCATGTTGGGCTTATCCT	719
Db	710	CCCCGATAGCTGTGGATGTGTGTGTTCATTTCCAGCATATATGTGGTGTCTATCCT	769
OY	720	GCCTGTATTGTCAATCCTGTCTCTGTCATTGCAATATCATCTCCAAAGCTGTCAACTCCAA	779
Db	770	GCCGGGCAATCGTCAATCCCTCTCTGTACTGCATCATCATCTCAAGCTGTCAACTCCAA	829
OY	780	GGGCGCACCAAGAGCGCAAGGCCCTCAAGACCAAGATCATCTCATCTGTGGTTCTTGGC	839
Db	830	GGGCGCACCAAGAGCGCAAGGCCCTCAAGAGCAAGATCATCTCATCTGTGGTTCTTGGC	889
OY	840	CTGTGGGTGCTTACATACATTTGGGATGGGATCAGATCGACCTCCATCCTCTGGAAATCAT	899
Db	890	CTGTGGGTGCTCATTATATGTGGGGATCAGATCGACCTCCATCCTCTTGTGGAGTCAAT	949
OY	900	CAAGCAAGGAGTGTAGTTTGAAGAACTGTGCACAAAGTGGATTTCCATCAGCAGAGGCCCT	959
Db	950	CAAGCAAGAGTGTAGTCTCGAGAGCAATGTGCACAAAGTGGATTTCCATCAGAGAGGCCCT	1009
OY	960	AGCTTTCTTCACTGTGTGTGAAAGCCCATCTCTATGCTTCTCTTGAGACCAATTTA	1011
Db	1010	CGCCTTTCTTCACTGTGTGCTGAAGCCCATCTCTATGCTTCTCTTGAGGCCCAAGTTCAA	1061
OY	1020	AACCTCTCCGAGCAGCACTCACTCTGTGAGAGAGGGGTCCAGGCTCAAGTCCCTGC	1071
Db	1070	AAGCTCTCCGAGATGACATCACTCATATGAGCAGAGGCTCCAGGCTCAAGATCTTTC	1121
OY	1080	CAAAAGAAAGCGAGGTGACATCTGTTTCCACTGAGCTGTGAGTCTTCAAGTTTTC	1131
Db	1130	CAAAAGAAAGCGGAGTGTGACACTCTTCGCTCCAGAGAGTCAAGAAATCCGCCAGTTTTC	1181
OY	1140	CTCCAGCTA-----CACAGATGTAAAGACTTTTTTATACGATTAATAACTTT	1191
Db	1190	CTCCAGCTAACCTTATGTCAAAGACTTATATATATATATATATATATATATATAAAGACTT	1241
OY	1192	TTTATAGTTACACTTTTTCGATATATAAGACAGACCAATATATGACGTTTATATTC	1251
Db	1250	TTTATGTATACACTTTTTCGAGATATAGAGACAGACCACTGTGTACAGTTTTTTTTT	1301
OY	1252	TGTGTGATTTTGT-----CTGTGTCTTTAGTTTGTGAGGATTAATGTACTTA	1301
Db	1310	TTTTTAATGTAGCTGTGGGAGATTTATGTCTCTAGTTTTTGTGAGGTTTGTACTTAATTT	1361
OY	1306	TTTATA---TAAATTTTTTTTGTTCATAATGATGTGTGTGAGCAGAGACCTGTGGCC	1361

Dd	1370	ATATAAATATTGTTTGTGGTTTGTTTCATGTGAATGAGCGCTTAGGAGAGACCTGTGGCC	1429
Oy	1362	AAGTCTTAGTGGTGTGATGCTGTGTGGTGTGACTGTAGAAAAG-----GCAGCTGA	1413
Dd	1430	AAGTCTTAGTAGTGTGTTTAATCTGTGTGAGACTGTAGAACGTGAGAGAACTGA	1489
Oy	1414	ACATTCACAGACCGGTGATGTGATCAGCTAAAGCTAGCAATGATCCCCAGCTGTTATGCA	1473
Dd	1490	ACATTCACGAAATGTGTGTAATGAAATGAAGCTGATGCCGATCTCAGCTGTGTCTGCA	1549
Oy	1474	TAGATAAATCTGTCCA-----	1489
Dd	1550	TAAATCTTTCATTTCCGAGAGACACCACCCACCCACCCACCCCATTTCTTAAT	1609
Oy	1489	-----TTCCC GTGAAACGTTTTTCCGTGCTTMAAGCGTGAAT	1525
Dd	1610	TGTTTGGTTATGCGTGTGATGATGGTTTGTGGTTTGTTTTGTGTTGTTGTTGTTT	1669
Oy	1526	TTTGCTGTAGAAGATGGCACTTATTAACCAAAGCCCAAGTGT-ATRGAATGCTGG---1582	
Dd	1670	TTTCTGTAAAAAGATGTGGCACTTAAACCAAAGCCTGAAAGTGTTGTAAGAAATCCTGGGGT	1729
Oy	1582	-----TTTTCAGTTTTCAGAGATGGGTGATTTTCAGACCTAC-AGT	1623
Dd	1730	TTTTTGTGTTGTTGTTTGTGTTTTCAGTTTTCAGAGATGATTTGACTTCAGTCCCTACAAAT	1789
Oy	1624	GTACAGTCTTGTTATTAAGTTGTTATTAAGTAAGTACATGTTAACTTAAAAAAAAAAAAAA	1683
Dd	1790	GTAAGCTGTGTATTAACATGTTGTAAATAAGTCAATGATTAACCTAAAAAAAAAAAAAA	1849
Oy	1684	AAAAAAAAAAAAAAAAAAAAAAAAAAAA1711	
Dd	1850	AAAAAAAAAAAAAAAAAAAAAAAAAAAA1877	
RESULT	8		
XI5883			
AC	XI5883 standard; cDNA; 611 BP.		
DT	12-MAY-1999 (first entry)		
DE	cDNA encoding a partial CXCR4B protein.		
KM	G-protein coupled receptor; CXCR4B; human; splice variant;		
KM	chemokine receptor; CXCR4; vaccine; gene therapy; HIV-1; HIV-1;		
KM	cancer; pain; diabetes; obesity; anorexia; bulimia; asthma;		
KM	Parkinson's disease; acute heart failure; hypotension; hypertension;		
KM	urinary retention; osteoporosis; angina pectoris; myocardial infarction;;		
KM	stroke; ulcer; allergy; benign prostatic hypertrophy; migraine;		
KM	vomiting; psychotic disorder; neurological disorder; anxiety;		
KM	schizophrenia; manic depression; delirium; dementia; mental retardation;		
KM	dyskinesias; Huntingtons disease; Gilles de la Tourette syndrome; ss.		
OS	Homo sapiens.		
PN	EP-897980-A2.		
PD	24-FEB-1999		
PF	07-AUG-1998; 306324.		
PR	24-JUL-1998; US-056601.		
PA	20-AUG-1997; US-056601.		
DR	(SMIK) SWITZERLINE BEECHAM CORP.		
PI	Gupta SK, Pillarisetti K;		
DR	WPL 99-134643/12.		
PT	P-PsDB; W97363.		
PT	New G protein coupled receptor (CXCR4B) polypeptide and		
PT	polynucleotide, human splice variant of a chemokine receptor -		
PT	useful as diagnostic reagents and for prevention and treatment of		
PT	HIV infection, cancer, stroke and dementia		
PS	Claim 13; Page 18; 24pp; English.		
CC	The present sequence encodes a partial G-protein coupled receptor		
CC	designated CXCR4B, which is a human splice variant of a chemokine		
CC	receptor CXCR4. CXCR4B polynucleotides and polypeptides are useful for		
CC	diagnosing susceptibility to diseases by detecting mutations or		
CC	polymorphisms in the CXCR4B gene or analyzing for the presence or amount		
CC	of CXCR4B polypeptide expressed in a patient. CXCR4B polypeptides and		
CC	polynucleotides are also useful for screening for antagonists and		


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OY 788 AGAAGCCGCAAGCCCTCAGACAGCAGTATCCATCTTGCGCTTCTTCCGTTGGC 847
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 829 AGAAGCAGCGGGCCATCGGGGTATCTTCCCGCTGCTCATCTTCTCTGCTGGC 888
OY 848 TGCCTTACTACATTTGGGATGAGCATGCTCTCTCATCTCTGAAATCATCAAGCAG 907
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 889 TGCCTTACAACTGTGCTCTCTGACAGACACCTCATGAGACCCAGTATCCAGAGAGA 948
OY 908 GGTGTAGTTGAGAACACCTGTGCACAGTGTATTTCCATTCACCGAGCCCTTACCTTCT 967
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 949 CGGTGAGCTGCGCAATGACATTTGACCGCGCCCTGAGCGCCAGATTTCTGGGCTTCC 1008
OY 968 TCCACTGTTGTGAAACCCCATCTATGCTTCTTCTTGAGCCAAATTT 1017
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1009 TGCACAGCTGCTCAGACCCCATCATCTACGCTTTCATTGGCCAAACTTT 1058

RESULT 12
ID 09951 standard; DNA; 1373 BP.
AC 09951:
DT 24-APR-1996 (first entry)
DE Recombinant high affinity Interleukin-8 receptor subtype B encoding DNA.
KW 11-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder;
KW anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis;
KW systemic necrotizing vasculitis; psoriasis; asthma; allergy; ARDS;
KW adult respiratory distress syndrome; neutrophil detection; ss.
OS Oryzctolagus cuniculus.
FT Key Location/Qualifiers
FT cds 71..1147
FT /tag= a
FT /product= IL-8B_receptor

WO9525126-A1.
PD 21-SEP-1995.
PF 09-MAR-1995; U03032.
PR 15-MAR-1994; US-210250.
PR 02-MAY-1994; US-237937.
PA (REPR ) REPLIGEN CORP.
PA (UYBO-) UNIV BOSTON.
PI Greenfield EA, Larosa GJ, Navarro J, Thomas KM;
PI Milt DT.
DR WPI: 95-336945/43.
DR P-PSDB: R80952.
PT Monoclonal antibody against recombinant IL-8 receptor polypeptide -
PT useful for treating inflammatory disorders, for detecting
PT neutrophil(s) and for isolating IL-8 receptor from liq.mixt.
PS Claim 6, Fig 3A-B, 74pp; English.
CC Monoclonal antibodies were raised against recombinant interleukin-8
CC (IL-8) receptor subtypes A and B from both human and rabbit sources
CC (R80950-53 encoded by 09949-52). The A subtype receptor (IL-8ra) is
CC a high affinity receptor and the B subtype receptor (IL-8rb) is a
CC low affinity receptor. The monoclonal antibody (mab) pref. binds to
CC the IL-8 binding domain thus blocking its activation. The mabs are
CC useful for treating inflammatory disorders (see key words) and for
CC detecting the presence of neutrophils in a biological sample. The
CC mabs are also useful in the isolation of IL-8 receptors from a mixture.
SQ Sequence 1373 BP; 266 A; 437 C; 329 G; 335 T;

Query Match 11.6%; Score 201.2; DB 1; Length 1373;
Best Local Similarity 54.8%; Pred. No. 4,6e-29;
Matches 467; Conservative 0; Mismatches 373; Indels 12; Gaps 3;

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DB 299 ACCTGCTGGTACAGCAGCTTACTGCTGAACTTGCCATGCGGACCTGCTCTTGGC 358
OY 355 ATACGCTTCCCTTTTGGGAGATTGATGCCGTGGCAACTGTGATTGGGAATTTCTTA 414
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 359 ACCACCTTGGCCATCTGGGGCCGCTCCAAAGTGCACAGGCTGGACATTTGGCAGCCCTTG 418
OY 415 TGCAGGAGTCCATGATCTCATCTACAGATCAACCTTACAGAGTGTCTCTCATCTGGCC 474
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 419 TGTAAAGTGTCTGCTTGTGAAGAAATCACTTACAGCGGAATCTGTCTGTGGCC 478
OY 475 TTGATAGTGTGAGCGCTACTACGCGCATGCTCCAGCCACCAAGCTGAGAGGCCAAG 534
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 479 TGTATAGTGTGAGCGCTACTACGCGCATGCTCCAGCCACCAAGCTGATGCCAAG 538
OY 535 AAGCTTTGGCTGAAAGAGTGTCTATGTTGGCGTGTGATCCCTGCTGCTGACT 594
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 539 CGCCACTTG---GTCAAAGTTCAATATCTTAAGCATGTGGGAGATGCTTGTATCTGTCT 595
OY 595 ATTCCGACTTCATCTTTGGCAAGTCAAGTGAAGCA---GATGACGATATATCTG---- 648
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 596 CTGCCATCTTACTGTTCCGTAAATGSCATCTTCCACCAATTCAGCCCGGCTGCTAT 655
OY 648 --TGACCGCTTACCCCAATGACTGTGGGTGTTGTCTTCAGTTTCAGCATCATG 705
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 656 GAGGACATGGGGAACAAGCACTGGGAATGGCGCATGTGCTGGGATCTGCTCAGACT 715
OY 706 GTTGGCTTATATCTGCTGTGATTTGATTCATCTGTCTGATTTGATTTATCTTCAAG 765
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 716 TTGGGCTTATCTGCTGCGGTGCTGTGATCTGTGTTGTGATGTGTTCAACCTGCGCAG 775
OY 766 CTGTCACTCCAAAGGCGCACAGAGCGGAGCGCCCTCAAGACACAGCATCTCTCAT 825
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 776 CTGTTCAGGCGCCATGSGGCAAGAGCACGGGCGCATGCGGTCTATCTTCCGCTGCTG 835
OY 826 CTGGCTTTCTTGGCTGTGGCTGCTCTTACTACATTTGGATCAGATCGATCTTCTATC 885
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 836 CTGATCTTCTTCTGTTGGGCTGCGCTTCAACCTGTGTCTGTGACAGACACCTCATG 895
OY 886 CTCTCGAATATCATCAAGCAAGGCTGTGATTTGAGAACACGTGTGACAAATGATTC 945
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 896 AGGACCCAGCTGATCCAGAGAGCTGTGAGCGCGGCAATGACATTCACGGGCGCTGAG 955
OY 946 ATCAGAGAGCCCTAGCTTCTTCCACTGTGTGCTGACCCCATCTCTATGCTTCTT 1005
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 956 GCGACCGAATTTGSGGCTTCTGTCACAGCTGCTCAACCCATCATCTACGCTTCAIT 1015
OY 1006 GGAGCCAAATTT 1017
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1016 GGCGAAAGTTT 1027
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 13
ID 029505 standard; DNA; 1933 BP.
AC 029505:
DT 12-MAR-1993 (first entry)
DE Interleukin-8 receptor
KW IL-8R; G-protein coupled receptor family; rhodopsin superfamily;
KW pro-inflammatory cytokine; ss.
OS Homo sapiens.
FT Key Location/Qualifiers
FT cds 51..1103
FT /tag= a
FT /product= IL-8R

WO9217497-A.
PD 15-OCT-1992.
PF 23-MAR-1992; U02317.
PF 29-MAR-1991; US-677211.
PR 19-DEC-1991; US-810782.
PA (GENE) GENENTECH INC.
PI Holmes WE, Lee J, Wood WI;
PI WPI: 92-366191/44.
P-PSDB: R27791.

```

PT Isolated human platelet factor 4 super-family receptor
 PT polypeptide and corresp. antibodies and DNA - useful as
 PT diagnostic and screening agents, and for treating inflammation or
 PF4R-mediated disorders
 PS Claim 7: Fig 2, 78pp, English.
 CC A cDNA library constructed from human neutrophil mRNA in the mammalian
 CC expression vector pRK5B was transfected into COS-7 cells as pools of
 CC 2500 clones. One positive pool from the first 58 transfections was
 CC partitioned into smaller pools until a pure clone (pRK5B.118r1.1)
 CC was obtained. The ORF encodes a protein of 350 amino acids which
 CC shares several features with the G-protein coupled receptors of the
 CC rhodopsin superfamily, including 7 hydrophobic (transmembrane)
 CC domains. See also Q29506 and Q37107.
 CC Sequence 1933 BP; 423 A; 541 C; 483 G; 486 T;
 S0

Query Match 11.3%; Score 196.8; DB 1; Length 1933;
 Best Local Similarity 53.9%; Pred. No. 3.2e-28;
 Matches 455; Conservative 0; Mismatches 377; Indels 12; Gaps 2;

QY 183 AGAAATGCTAATTTCAATAAATCTTCCTGCCACATCTCCATCATCTTTTAA 242
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 146 AGAACTAGACACTCAACAAATATGTGTATCATCCCTATGCCCTTAGTCTCT 205
 QY 243 TGGCATTTGGGCAATGATTTGGTATCCTCGTCAATGGGTTACAGAAATCTAGAAG 302
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 206 GAGCTCTGGGAAACTCCCTGGTATGTATGCTGATCTTATACAGAGAGTGGCGCTC 265
 QY 303 CATGACGCAAGTACAGGCTGCACCTGTCAATGGCCACCTCCCTTTGTATACGCT 362
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 266 GGTCACTATGTCTACCTGTGAACCTGGCTGGCCGACACTCTTTGGCCCTACCTT 325
 QY 363 TCCCTTTGGGCAATGATGCGGTGCAAACTGTACTTTGGGAACTTCTATGCAAGC 422
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 326 GCCATCTGGGGCGGCTCCAGATGATGGCGATTTTGGCAATTCCTGTGAAGT 385
 QY 423 AGTCATATCTATCAACAGTCAACCTCTACAGAGTGTCTCTATCTGGCCCTTATAG 482
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 386 GGTCTACTCTCTGAAGAGTCAACTTCTACAGTGGATCCGCTGTGGCTGATCAG 445
 QY 483 TGTGACCGGCTACCTGGGCTATGCTCCAGCCCAACAGTACAGGCCAAGAGCTTT 542
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 446 TGTGACCGGCTACCTGGGCTATGCTCCAGCCCAACAGTACAGGCCAAGAGCTTT 505
 QY 543 GGGTGAAGAGTGTCTATGTTGGCTGTGATCCCTCCCTCTGATATTCACCGA 602
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 506 G---GTCAAGTTGTTTGTCTGGCTGGGACTGTCTATGATCTGTCCCTGCTT 562
 QY 603 CTTCATCTTTGCCAAGTCAAGTGAAGAGATGATATATCTGT-----GACCG 653
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 563 CTTCCTTTCCGCGAGCTTACATCAACAATCCAGTCCAGTTGCTATGAGAGTCT 622
 QY 654 CTTCACCCCAATGACTGTGGGTGTGTGTTCCAGTTTACAGCATCATGTTGGCT 713
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 623 GGGAAATACACAGAAATGGCGATGTGTGGATCTGCTCACCCTTGGGCTT 682
 QY 714 TATCTGCTGATATTTGATCTCTCTGATATGATATATCATCTCAAGCTTACA 773
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 683 CATGTGCGGCTGTTGTGATGCTGTCTGTATGATATCACTGCGGTAACTGTTAA 742
 QY 774 CTCCAAGGCAACAGAGCGCAAGCCCTCAAGACAGTCACTCATCTGCTGCTT 833
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 743 GGGCCACATGAGGAGAGACCGGATGAGGTATCTTTGTGTGTCGTCATCTT 802
 QY 834 CTTCGCTGTTGGCTGCTTACTATGATGAGATCAAGTCACTCTTATCTCTGGA 893
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 803 CTCTGTTGCTGGCTGCTCAACCTGCTGCTGCAACACCTCATGAGAGACCA 862
 QY 894 AATCAACGCAAGGTTGATGAGACAGTGTGACAGTGTGACAGTGTGATTCATCAG 953
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 863 GGTGATTCAGAGACTGTGAGCACCAGCAACATCGCGGCGGCTGTGATGCTCAG 922
 QY 954 GGCCTAGCTTTTCCACTGTGTGTGTAACCCATCTCTATGCTTCTTGGAGCCA 1013

Db 923 GATCTGGGATTTCCATACCTGCTCAACCCCATCATCTAGCCCTTACCGCAAA 982
 QY 1014 ATTT 1017
 ||||
 Db 983 TTTT 986

RESULT 14
 ID 080520 standard; cDNA; 1933 BP.
 AC 080520;
 DT 18-JUL-1995 (first entry)
 DE Interleukin-8 receptor cDNA insert.
 KW Interleukin-8 receptor; IL-8 receptor; PF4R;
 KW platelet factor superfamily receptor; neutrophil; chemotactic;
 KW inflammation; inflammatory disease; arthritis; emphysema; cystic;
 KW fibrosis; colitis; bronchitis; meningitis; therapeutic; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT cds 51, 1103
 FT /tag- a
 PN W09428931-A.
 PD 22-DEC-1994.
 PF 07-JUN-1994; U06380.
 PR 11-JUN-1993; US-076093.
 PA (GETH) GENENTECH INC.
 PI Chuntarapai A, Hebert C, Kim KJ, Lee J;
 DR WPI: 95-036114/05.
 DR P-PSDB: R68811.
 PT Treatment of inflammatory disorders - by administering an
 PT antibody capable of binding a platelet factor 4 superfamily
 PT receptor polypeptide
 PS Disclosure, Page 51-54; 83pp; English.
 CC A cDNA library constructed from human neutrophil mRNA in pRK5B was
 CC transfected into COS-7 cells, and the cells were screened with 125I-
 CC IL-8. The DNA sequence of isolated cDNA clone pRK5B.118r1.1,
 CC encoding human IL-8 receptor, is given in 080520 and the predicted
 CC amino acid sequence in R68811. The receptor is used to raise
 CC antibodies that neutralize the activity of PF4R, e.g. IL-8 receptor.
 SQ Sequence 1933 BP; 422 A; 540 C; 485 G; 486 T;

Query Match 11.3%; Score 196.8; DB 1; Length 1933;
 Best Local Similarity 53.9%; Pred. No. 3.2e-28;
 Matches 455; Conservative 0; Mismatches 377; Indels 12; Gaps 2;

QY 183 AGAAATGCTAATTTCAATAAATCTTCCTGCCACATCTCCATCATCTTTTAA 242
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 146 AGAACTAGACACTCAACAAATATGTGTATCATCCCTATGCCCTTAGTCTCT 205
 QY 243 TGGCATTTGGGCAATGATTTGGTATCCTCGTCAATGGGTTACAGAAATCTAGAAG 302
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 206 GAGCTCTGGGAAACTCCCTGGTATGTATGCTGATCTTATACAGAGAGTGGCGCTC 265
 QY 303 CATGACGCAAGTACAGGCTGCACCTGTCAATGGCCACCTCCCTTTGTATACGCT 362
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 266 GGTCACTATGTCTACCTGTGAACCTGGCTGGCCGACACTCTTTGGCCCTACCTT 325
 QY 363 TCCCTTTGGGCAATGATGCGGTGCAAACTGTACTTTGGGAACTTCTATGCAAGC 422
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 326 GCCATCTGGGGCGGCTCCAGATGATGGCGATTTTGGCAATTCCTGTGAAGT 385
 QY 423 AGTCATATCTATCAACAGTCAACCTCTACAGAGTGTCTCTATCTGGCCCTTATAG 482
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 386 GGTCTACTCTCTGAAGAGTCAACTTCTACAGTGGATCCGCTGTGGCTGATCAG 445
 QY 483 TGTGACCGGCTACCTGGGCTATGCTCCAGCCCAACAGTACAGGCCAAGAGCTTT 542
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 446 TGTGACCGGCTACCTGGGCTATGCTCCAGCCCAACAGTACAGGCCAAGAGCTTT 505
 QY 543 GGGTGAAGAGTGTCTATGTTGGCTGTGATCCCTCCCTCTGATATTCACCGA 602
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 506 G---GTCAAGTTTGTGTTGCTTGCTGCTGGGAGACTGTCTATGATCTGTCCCTG 562
QY 603 CTTATCTTTTCCCAAGCTGAGGAGATGACGATATATCTGT-----GACCG 653
Db 563 CTTCTTTTCCGACAGGCTTACATCCAAACATTCACAGTTCATGAGTCT 622
QY 654 CTTTACCCCAATGACTGTGGTGTGTGTTCCAGTTTACGACATCATGTTGGCT 713
Db 623 GGGAAATACACAGCAAAATGCGGATGTGTGGGATCTCTGCTCACACCTTTGGCTT 682
QY 714 TATCTGCTGCTGATTTGATCTCTGCTGATTTGATTTATCATTCACCAAGTGTACA 773
Db 683 CATGCTGCGCTGTTGTTCATGCTGTCTGCTATGATTCACCTGGCTTACACTTTAA 742
QY 774 CTCGAGGGCCACAGAGGCGCAAGGCTTCAAGCCACAGTCACTCTCATCTTGGCTT 833
Db 743 GGGCCACATGGGAGAGACCGACCGCATGAGGCTCATCTTGTCTGCTCATCTT 802
QY 834 CTTGCGCTGCTGCTGCTTACTACTATGGATGGATGAGTCACTGCTTCTCTGCTGGA 893
Db 803 CTTGCTTGTGCTGCTGCTGCTTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 862
QY 894 AATCATCAGCAGAGGCTGTGATTTGAGACACTGTGCAACAAGTGTTCATCACCAG 953
Db 863 GGTGATCCAGAGACCTGTGAGAGCGCCGCAACATCGCGGCGCTGATGCACTGA 922
QY 954 GGCCTTACTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1013
Db 923 GATCTGGGATTTCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 982
QY 1014 ATTT 1017
Db 983 TTTT 986

RESULT 15
Q99006
ID 099006 standard; cDNA; 1883 BP.
AC 099006;
DT 26-MAR-1996 (first entry)
DE Interleukin 8 receptor A cDNA insert.
KW Interleukin; IL-8; Inflammation; psoriasis; dermatitis;
KW Rheumatoid arthritis; inflammatory bowel disease;
KW Chronic lung inflammation; treatment; antibody;
KW Affinity purification; detection; ss.
OS Homo sapiens.
PN USS440021-A.
PD 08-AUG-1995.
PF 29-MAR-1991; 677211.
PR 29-MAR-1991; US-677211.
PR 25-FEB-1994; US-202056.
PA (CHUN/) CHUNTHARAPAI A.
PA (HEBE/) HERBERT C.
PA (KIMK/) KIM K J.
PI (LEU/) LEE J.
PI Chuntharapai A, Hebert C, Kim KJ, Lee J;
DR WPI: 95-283151/37.
DR P-PSDB: R80756.
PT New antibodies against interleukin 8 type B receptor - used to treat
PT or prevent inflammation, also for detecting receptor expression and
PT purification.
PS Example 2: Columns 43-46; 62pp; English.
CC Antibodies directed against the interleukin-8 receptor B can be used
CC to treat or prevent inflammation e.g. psoriasis, dermatitis.
CC rheumatoid arthritis and particularly inflammatory bowel disease and
CC chronic lung inflammation. When immobilised, these antibodies may
CC be used to detect interleukin-8 receptor B expression in cells and
CC tissues and for affinity purification of interleukin-8 receptor B
CC from cells. A sequence obtained from this cDNA insert, which
CC encodes the high affinity interleukin-8 receptor, was used to
CC probe lambda gt10 cDNA libraries for the human interleukin-8
CC type B receptor.
SQ Sequence 1883 BP; 408 A; 528 C; 472 G; 475 T;

Query Match 11.3%; Score 196.8; DB 1; Length 1883;
Best Local Similarity 53.9%; Pred. No. 3.2e-28;
Matches 455; Conservative 0; Mismatches 377; Indels 12; Gaps 2;
QY 183 AGAAAATGCTAATTTCAATTAATAATCTTCCGCGCCACATCTACTTCATCTTTTAC 242
Db 96 AGAAACTGAGACACTCAACAAGATGTTGATGATGCTATGACCTATGCTAGTTCCTGCT 155
QY 243 TGGCATTTGGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 302
Db 156 GAGCTGTGGGAAATCTCCGTTGATGATGATGATGATGATGATGATGATGATGATGAT 215
QY 303 CATACGAGCAATGACAGGCTGACCTGTGAGTGGCGGACCTCTCTTGTTCATCAGCT 362
Db 216 CGTACATGATGTCTACTGCTGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 275
QY 363 TCCCTTGGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 422
Db 276 GCGCATGCGGCGCTCCAGAGTGAATGCTGATTTTGGACATTCCTGTGCAAGT 335
QY 423 AGTCATGTCTATCTACACAGCTCTACAGCAGTGTCTCTATCTGCTGCTCATCAG 482
Db 336 GGTCTCACTCTCTGAGGAAAGTCACTTCTACAGTGGATCTCTGTTGGCTGCTCATCAG 395
QY 483 TCTGACCGCTACTCTGCGCATCTGTCACGCCACCAAGTGTGAGGCGCAAGAGTGT 542
Db 396 TGTGAGCGTTACTCTGCGCATCTGTCATGTCACACGACACTGACCAAGAGCTACTT 455
QY 543 GCGTGAAGAGTGTCTATGTTGGCTGCTGATGCCCTGCTGCTGCTGCTGCTGCTGCTG 602
Db 456 G---GTCAAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 512
QY 603 CTTGATCTTTECCACAGCTCAAGTGGAGATGACAGATATATCTGT-----GACCG 653
Db 513 CTTCTTTTCCGACAGGCTTACCATCCAAACATTCAGTTCATGCTGATAGTGCT 572
QY 654 CTTTACCCCAATGATCTTGTGGTGTGTGTTTCACTTTGACACATCATGTTGGCTT 713
Db 573 GGGAAATGACACAGCAAAATGGCGGATGTGCTGCGATCTGCTGCTGCACTTTGGCTT 632
QY 714 TATCTGCTGCTGATTTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 773
Db 633 CATGCTGCGCTGTTGTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 692
QY 774 CTCGAGGGCCACAGAGGCGCAAGGCGCTCAAGCCACAGTCACTCTCACTGCTT 833
Db 693 GCGCCACATGGGAGAGAGACCGAGCCATGAGGATCATCTTGTGCTGCTGCTCATCTT 752
QY 834 CTTGCGCTGTTGGTGGCTTACTATGATGATGATGATGATGATGATGATGATGATGAT 893
Db 753 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 812
QY 894 AATCATCAGCAGAGGCTGTGATTTGAGACACTGTGCAACAAGTGTTCATCACCAG 953
Db 813 GGTATCCAGAGACCTGTGATGAGGCGCCGCAACATGCGCGGCTGATGCTGCTGCTG 872
QY 954 GGCCTTACTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1013
Db 873 GATCTGGGATTTCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 932
QY 1014 ATTT 1017
Db 933 TTTT 936

Search completed: September 14, 1999, 10:07:50
Job time: 845 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 14, 1999, 09:52:23 : Search time 465.14 Seconds
(without alignments)
11876.419 Million cell updates/sec

Title: US-09-104-063-3

Sequence: 1 GAATTCACAGTGTCTGGCGG.....CCGCCACACACTGGAATTC 1737

Scoring table: IDENTITY_NUC

Searched: 679419 seqs, 1590154680 residues

Database :

GenEmbl.*
1: gb_dal.*
2: gb_da2.*
3: gb_om.*
4: gb_ov.*
5: gb_pat.*
6: gb_ph.*
7: gb_pl.*
8: gb_pl2.*
9: gb_pr1.*
10: gb_pr2.*
11: gb_pr3.*
12: gb_ro.*
13: gb_st.*
14: gb_sy.*
15: gb_sy.*
16: gb_un.*
17: gb_vl.*
18: em_fun.*
19: em_hgt.*
20: em_hum1.*
21: em_hum2.*
22: em_in.*
23: em_om.*
24: em_or.*
25: em_ov.*
26: em_pat.*
27: em_ph.*
28: em_pl.*
29: em_ro.*
30: em_sts.*
31: em_sy.*
32: em_un.*
33: em_vl.*
34: gb_hgtl.*
35: gb_hgt2.*
36: gb_in1.*
37: gb_in2.*
38: em_ba1.*
39: em_da2.*
40: em_hum3.*
41: em_hum4.*
42: gb_pr4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	1737	100.0	1737	5	ARO15970 Sequence

2	1737	100.0	1737	5	113753	113753 Sequence 4
3	1737	100.0	1737	5	124455	124455 Sequence 3
4	1653.4	95.2	1664	9	HUMHM89	D10924 Human mRNA
5	1653.4	95.2	1664	14	G28514	G28514 Human STS S
6	1642	94.5	1645	10	HSNRYRLA	X71635 H.sapiens m
7	1625.2	93.6	1670	9	HUMGPCR	L06797 Human (clon
8	1564	90.0	5161	11	AF005058	AF005058 Homo sapi
9	1562.4	89.9	8747	9	HSZA224869	AJ242869 Homo sapi
10	1562.4	89.9	8747	11	AF052572	AF052572 Homo sapi
11	1556.4	89.4	1637	9	HUMGSTR	M99293 Homo sapien
12	1536	88.4	3733	10	HSCXCR4	Y14739 Homo sapien
13	1266.6	72.9	1689	3	FCAS816	AJ008816 Felis cat
14	1213	69.8	1225	9	HUMNTRPCA	L01639 Human (clon
15	1084.6	62.4	1126	11	AF019378	AF019378 Cercopith
16	1083.8	62.4	1087	11	PT089798	U89798 Pan troglod
17	1059	61.0	1059	11	AF025375	AF025375 Homo sapi
18	1048.6	60.4	1087	11	AF001928	AF001928 Macaca mu
19	1042.8	60.0	1078	9	D86579	D86579 Macaca fasc
20	1027	59.1	1059	11	AF031089	AF031089 Papio ham
21	1024.8	59.0	1068	9	AB015943	AB015943 Chloroceb
22	1020.6	58.8	1059	10	MMU93311	U93311 Macaca mula
23	1020.6	58.8	1059	11	MMU73740	U73740 Macaca mula
24	1007.8	58.0	1059	11	AF051906	AF051906 Cercopetu
25	998.4	57.5	1280	3	BOVNYR	M86739 Cow neurope
26	974.4	56.1	1877	12	D87747	D87747 Mus musculu
27	950.6	54.7	1170	3	FCU63538	U63538 Felis catus
28	936.8	53.9	1575	12	MMLESTRPT	X99582 M.musculus
29	935.8	53.9	1809	12	AB000803	AB000803 Mouse mRN
30	923.6	53.2	3770	12	MMLESTRGN	X99581 M.musculus
31	914.2	52.6	1140	3	FCU92795	U92795 Felis catus
32	846.4	48.7	1223	12	MMU59760	U59760 Mus musculu
33	845.8	48.7	1422	12	MMLCR13	Z80113 Mus musculu
34	844.4	48.6	1180	12	MMLCR12	Z80112 Mus musculu
35	804.6	46.3	3366	12	MMU65580	U65580 Mus musculu
36	804	46.3	1050	12	RNU90610	U90610 Rattus norv
37	762.2	43.9	1362	12	RNU54791	U54791 Rattus norv
38	545	31.4	2090	4	XLA17894	Y17894 Xenopus lae
39	542.8	31.2	2264	4	XLA17895	Y17895 Xenopus lae
40	462.8	26.6	378	3	OAUX8942	U38942 Ovis aries
41	433.6	25.0	1681	4	OMCXCRC	AJ001039 Oncomyrnc
42	398	22.9	1632	4	AB012310	AB012310 Cyprinus
43	377.4	21.7	528	12	MMLCR11	Z80111 Mus musculu
44	206.8	11.9	1068	3	RAB1L8C	M74240 Oryctolagus
45	206.8	11.9	1232	3	RAB1L8BRC	M82873 Oryctolagus

ALIGNMENTS

RESULT 1	ARO15970	1737 bp	DNA	PAT	04-DEC-1998
LOCUS	ARO15970	Sequence 3 from patent US 5776457.			
DEFINITION	ARO15970				
ACCESSION	93972247				
NID	93972247				
VERSION	ARO15970.1	GI:3972247			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 1737)				
AUTHORS	Lee J. and Wood W. I.				
TITLE	Antibodies to human PFA4 receptor and compositions thereof				
JOURNAL	Patent: US 5776457-A 3 07-JUL-1998;				
FEATURES	Location/Qualifiers				
source	1..1737				
BASE COUNT	454 a 411 c 373 g 499 t				
ORIGIN	/organism="unknown"				
Query Match	100.0%;	Score 1737;	DB 5;	Length 1737;	
Best Local Similarity	100.0%;	Pred. No. 0;			

Matches 1737: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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OY 1 GAATTCACATGTCGCGCGCGCGCAAGTACGCGCGGCGCTGAGTGCACGTA 60
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Db 1561 AAAGTGTATGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
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Db 1621 AGTGTACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
OY 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1737
Db 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1737

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RESULT 2

LOCUS	113753	1737 bp	DNA	PAT	18-SEP-1995
DEFINITION	Sequence	4 from patent	US 5440021.		
ACCESSION	113753				
VERSION	9996819				
KEYWORDS	113753.1	GI:996819			
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1737)				
AUTHORS	Chuncharapal, A., Hebert, C., Kim, K.J. and Lee, J.				
TITLE	Antibodies to human IL-8 type B receptor				
JOURNAL	Patent: US 5440021-A 4 08-Aug-1995;				
FEATURES	Location/Qualifiers				
SOURCE	1..1737				
BASE COUNT	454 a 411 c 373 g 499 t				
ORIGIN					

Query Match 100.0%; Score 1737; DB 5; Length 1737;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1737: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

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Db 841 TGTGCTGCTCTACTACATTTGGGATGAGATGAGATGAGATGAGATGAGATGAGAT 900
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Db 1081 AAAGGAAGGAGGTGACATTCATCTGTTCCAGTGTGAGTTCAGATTTTCCAC 1140

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RESULT 3
LOCUS 124455 1737 bp DNA PAT 14-AUG-1996
DEFINITION Sequence 3 from patent US 5543503.
ACCESSION 124455
NID 51604325
VERSION 124455.1 GI:1604325
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1737)
AUTHORS Chuntcharapai, A., Lee, J., Hebert, C. and Kim, K. Jin.
TITLE Antibodies to human IL-8 type A receptor
JOURNAL Patent: US 5543503-A 3 06-AUG-1996.
FEATURES
source
BASE COUNT 454 a 411 c 373 g 499 t
ORIGIN

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Query Match 100.0%; Score 1737; DB 5; Length 1737;
Best local Similarity 100.0%; Pred. No. 0;
Matches 1737; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 GAATTCAGTGTGCTGGCGGCGCGCAAGTGAAGCGCGAGGCGCTGAGTCTCCAGTA 60
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RESULT 4
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DEFINITION Human mRNA for HM89.
ACCESSION D10924
VERSION 9219868
D10924.1 GI:219868
KEYWORDS GTP-binding protein; plasma membrane protein; protein coupled.
SOURCE Homo sapiens monocyte, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1664)
AUTHORS Nomura,H., Nielsen,B.W. and Matsushima,K.
TITLE Molecular cloning of cDNAs encoding a LD78 receptor and putative
leukocyte chemotactic peptide receptors
JOURNAL Int. Immunol. 5 (10), 1239-1249 (1993)
MEDLINE 94092629
COMMENT Submitted (13-Apr-1992) to DDBJ by:
Hideki Nomura
Dept. of Pharmacol.
Cancer Res. Inst., Kanazawa Univ.
13-1 Takaramachi
Kanazawa, Ishikawa 920
Japan
Phone: 0762-62-8151 x5875
Fax: 0762-60-7704.
FEATURES
Location/Qualifiers
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SOURCE human.
 ORGANISM Homo sapiens
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 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1664)
 AUTHORS Myers, R.M.
 JOURNAL Unpublished (1996)
 COMMENT

Contact: Richard M. Myers
 Stanford Human Genome Center (SHGC)
 Stanford University School of Medicine
 Department of Genetics, M-344, Stanford, CA 94305, USA
 Tel: 4157259687
 Fax: 4157259689
 Email: myerseshgc.stanford.edu

Primer A: TTGTACAGTCTTTATGCTGTG
 Primer B: CGTATTAATACACGCTCTGG
 STS size: 207
 PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds
 Annealing: 62 degrees C for 23 seconds
 Polymerization: 72 degrees C for 30 seconds
 PCR Cycles: 30
 Thermal Cycler: Perkin Elmer 9600

Protocol: Template: 25 ng
 Primer: each 1 uM
 dNTPs: each 200 uM
 Taq Polymerase: 0.05 units/ul
 Total Vol: 10 ul

Buffer: MgCl2: 2.5 mM
 KCl: 50 mM
 Tris-HCl: 20 mM
 pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from D10924
 -- Washington University/Merck EST sequence.

FEATURES
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 Location/Qualifiers
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 /db_xref="taxon:9606"
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 complement(1405..1426)
 BASE COUNT 414 a 398 c 359 g 493 t
 ORIGIN

Query Match 95.2%; Score 1653.4; DB 14; Length 1664;
 Best Local Similarity 99.6%; Pred. No. 5,6e-290;
 Matches 1657; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DEFINITION	H.sapiens mRNA for neuropeptide Y-like receptor.	PRI	15-FEB-1994
ACCESSION	X71635		
KEYWORDS	g297099		
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SOURCE	Chemotaxis; G-protein coupled receptor; neuropeptide Y. human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukariota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1645)		
AUTHORS	Moser, B.		
TITLE	Direct Submission		
JOURNAL	Submitted (26-APR-1993) B. Moser, University of Bern, PO Box 99, Bern, SWITZERLAND		
REFERENCE	2 (bases 1 to 1645)		
AUTHORS	Loetscher, M., Geisler, T., O'Reilly, T., Zahlen, R., Baggiolini, M., and Moser, B.		
TITLE	Cloning of a human seven-transmembrane domain receptor, LESTR, that is highly expressed in leukocytes		
JOURNAL	J. Biol. Chem. 269 (1), 232-237 (1994)		
MEDLINE	94103215		
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DEFINITION		Human (clone L5) orphan G protein-coupled receptor mRNA, complete cds.	
ACCESSION		L06797	
NID		9414929	
VERSION		L06797.1 GI:414929	
KEYWORDS		G protein-coupled receptor; neuropeptide receptor.	
SOURCE		Human adult lung cDNA to mRNA.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS		1 (bases 1 to 1670)	
TITLE		Herzog, H., Hort, Y.J., Shine, J. and Selbie, L.A.	
JOURNAL		Molecular cloning, characterization, and localization of the human homolog to the reported bovine NPY Y3 receptor: lack of NPY binding and activation	
MEDLINE		DNA Cell Biol. 12, 465-471 (1993)	
COMMENT		93319629	
FEATURES		On Nov 10, 1993 this sequence version replaced gi:414927.	
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VERSION AF005058.1 GI:2735718
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SOURCE Homo sapiens
ORGANISM Homo sapiens

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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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1 (bases 1 to 5161)
Wegner,S.A., Ehrenberg,P.K., Chang,G., Dayhoff,D.E. and
Michael,N.L.
Genomic organization and characterization of the promoter for the
HIV-1 entry co-receptor CXCR-4
Unpublished
2 (bases 1 to 5161)
Wegner,S.A., Ehrenberg,P.K., Chang,G., Dayhoff,D.E. and
Michael,N.L.
Direct Submission
Submitted (21-MAY-1997) Division of Retrovirology, Walter Reed Army
Institute of Research, 13 Talt Court, Suite 200, Rockville, MD
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 Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 8747)
 AUTHORS Caruz, A.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAR-1998) Caruz A., Immunologie Virale, Institut
 Pasteur Paris, 28 Rue Dr. Roux Paris Cedex 15, 75724, FRANCE
 REFERENCE 2 (bases 1 to 8747)
 AUTHORS Caruz, A., Sansom, M., Alonso, J. M., Alcamí, J., Balleux, F.,
 Virelizier, J. L., Parmentier, M., and Arenzana-Seisdedos, F.
 TITLE Genomic organization and promoter characterization of human CXCR4
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 JOURNAL FEBS Lett. 426 (2), 271-278 (1998)
 MEDLINE 98258970
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 REFERENCE 1 (bases 1 to 8747)
 AUTHORS Caruz, A., Samsom, M., Alonso, J. M., Alcamí, J., Balazs, F.,
 Virelizier, J. L., Parmentier, M. and Arenzana-Seisdedos, F.
 TITLE gene
 JOURNAL FEBS Lett. 426 (2), 271-278 (1998)
 MEDLINE 98258970
 REFERENCE 2 (bases 1 to 8747)
 AUTHORS Caruz, A., Samsom, M., Virelizier, J. L., Parmentier, M. and
 Arenzana-Seisdedos, F.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAR-1998) Immunologie Virale, Institut Pasteur, 28
 Rue Dr Roux, Paris 75724, France
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VERSION 9292516
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AUTHORS Federerpiel, B., Melhado, I. G., Duncan, A. M., Delaney, A.,
Schapercl, K., Clark-Lewis, I. and Jirik, F. R.
TITLE Molecular cloning of the cDNA and chromosomal localization of the
gene for a putative seven-transmembrane segment (7-TMS) receptor
isolated from human spleen
JOURNAL Genomics 16, 707-712 (1993)
MEDLINE 93315164
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 ORGANISM Homo sapiens
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 REFERENCE 1 (bases 1 to 3733)
 AUTHORS Froidl, R., Moepf, B. and Gierschik, P.
 TITLE Genomic organization and expression pattern of the human chemokine
 receptor CXCR4
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 3733)
 AUTHORS Froidl, R.
 TITLE Direct Submission
 JOURNAL Submitted (03-SEP-1997) R. Froidl, Department of Pharmacology and
 Toxicology, Albert-Einstein-Allee 11, University of Ulm, 89081 Ulm,
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		Eutheria; Carnivora; Fissipedia; Felidae; Felis.							

REFERENCE	1 (bases 1 to 1689)
AUTHORS	Kovacs,E.M., Baxter,G.D. and Robinson,W.F.
TITLE	Feline peripheral blood mononuclear cells express message for both CXC and CC type chemokines
JOURNAL	Arch. Virol. 144, 273-285 (1999)
REFERENCE	2 (bases 1 to 1689)
AUTHORS	Kovacs,E.M.
TITLE	Direct Submission
JOURNAL	Submitted (27-JUL-1998) Kovacs E.M., Department of Medicine, The Princess Alexandra Hospital, First Floor, Lions Research Unit, Ipswich Road, Woolloongabba, 4102, AUSTRALIA
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SOURCE	1. .1689

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NID	94102931		
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	Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae;		
	Chlorocebus.		
REFERENCE	1 (bases 1 to 1126)		
AUTHORS	Holtkamp, N., Bailer, M. and Werner, A.		
TITLE	CXCR4 from African green monkey		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1126)		
AUTHORS	Holtkamp, N., Bailer, M. and Werner, A.		
TITLE	Direct Submission		
JOURNAL	Submitted (14-AUG-1997) 6/3, Paul-Ehrlich-Institut, Paul-Ehrlich-Str.51-59, Langen 63225, Germany		
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1141 TCCAGCTAACAAGATTAAGACTTTTATATACGATTAATTAATCTTTTAAAGT 1200
1141 TCCAGCTAACAAGATTAAGACTTTTATATACGATTAATTAATCTTTTAAAGT 1200
1201 ACACATTTTTCAGATATAAAGACTGACCAATATTGATGATTTTATGCTTGTGAT 1260
1201 ACACATTTTTCAGATATAAAGACTGACCAATATTGATGATTTTATGCTTGTGAT 1260

1201 ACACATTTTTCAGATATAAAGACTGACCAATATTGATGATTTTATGCTTGTGAT 1260
1261 TTTGTCTGTGTTCTTCTTACTTTTGTGAAGTTAATGACTTATTAATTAATTTT 1320
1261 TTTGTCTGTGTTCTTCTTACTTTTGTGAAGTTAATGACTTATTAATTAATTTT 1320
1321 TTTGTCTGTGTTCTTCTTACTTTTGTGAAGTTAATGACTTATTAATTAATTTT 1380
1321 TTTGTCTGTGTTCTTCTTACTTTTGTGAAGTTAATGACTTATTAATTAATTTT 1380
1381 GTCTGCTGTGAGTGTAGAGGAAAGGAACTGAACATCTCCAGACGTTGATGATCAG 1440
1381 GTCTGCTGTGAGTGTAGAGGAAAGGAACTGAACATCTCCAGACGTTGATGATCAG 1440
1441 TAAAGCTGAATGATCCCGAGCTGTTATGATGATGATGATGATGATGATGATGAT 1500
1441 TAAAGCTGAATGATCCCGAGCTGTTATGATGATGATGATGATGATGATGATGAT 1500
1501 GTTTTCTGTTCTTAAAGCTGATTTTGTGTAAGATGAGCACTTATTAACCAAGCC 1560
1501 GTTTTCTGTTCTTAAAGCTGATTTTGTGTAAGATGAGCACTTATTAACCAAGCC 1560
1561 AAAGTGTATGAATGCTGTTTTCAGTTTTCAGAGTGGTGTGATTTGACACCTAC 1620
1561 AAAGTGTATGAATGCTGTTTTCAGTTTTCAGAGTGGTGTGATTTGACACCTAC 1620
1621 AGTGTACGCTGTGATTAATTTGATTAATTAATTAATTAATTAATTAATTAATTA 1680
1621 AGTGTACGCTGTGATTAATTTGATTAATTAATTAATTAATTAATTAATTAATTA 1680
1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCGACACACTGGAATTC 1737
1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCGACACACTGGAATTC 1737

RESULT 2
US-08-076-093A-3
Sequence 3, Application US/08076093A
Patent No. 5543503
GENERAL INFORMATION:
APPLICANT: Chunharapal, Anan
APPLICANT: ~~Lee, James~~
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PFA4 Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/222-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 nucleotides
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-076-093A-3

Query Match	Similarity	100.0%	Score 1737	DB 1	Length 1737
Best Local	Similarity	100.0%	Pred. No. 0		
Matches 1737	Conservative	0	Mismatches	0	Indels
					Gaps
QY 1	GAATTCAGTGTGCTGGCGGCGCGGCGGCAAGATGACGCCGAGGGCTGAGTCTCCAGTA	60			
Db 1	GAATTCAGTGTGCTGGCGGCGCGGCGGCAAAATGACGCCGAGGGCTGAGTCTCCAGTA	60			
QY 61	GCCACCGCATCTGGAGAACCCAGCGGTTACCATGAGAGGGATAGATATATACACTCAGAT	120			
Db 61	GCCACCGCATCTGGAGAACCCAGCGGTTACCATGAGAGGGATAGATATATACACTCAGAT	120			
QY 121	AACTACACCGAGGAATGGGCTCAGGGGACATATGACTCCATGAAGAAACCGTGTTCGT	180			
Db 121	AACTACACCGAGGAATGGGCTCAGGGGACATATGACTCCATGAAGAAACCGTGTTCGT	180			
QY 181	GAGAGAAATGCTAATTTCAATTAATCTTCTCGCCACCACATCTACTCCATATCTTCTTA	240			
Db 181	GAGAGAAATGCTAATTTCAATTAATCTTCTCGCCACCACATCTACTCCATATCTTCTTA	240			
QY 241	ACTGGCATTTGGGGCAATGAGATGGTGCATCCGTCATAGGGGTTTACAGAGAAACTGAGA	300			
Db 241	ACTGGCATTTGGGGCAATGAGATGGTGCATCCGTCATAGGGGTTTACAGAGAAACTGAGA	300			
QY 301	AGCATGACGAGCAAGTACAGAGGCTGCACCTGTTCAGTGGCCGACCTCTCTTTGTCAACG	360			
Db 301	AGCATGACGAGCAAGTACAGAGGCTGCACCTGTTCAGTGGCCGACCTCTCTTTGTCAACG	360			
QY 361	CTTCCCTCTTGGGGCGATTGATGGCGGTGGCAAACTGGTACTTTGGGAACATCCTATGGCA	420			
Db 361	CTTCCCTCTTGGGGCGATTGATGGCGGTGGCAAACTGGTACTTTGGGAACATCCTATGGCA	420			
QY 421	GCAGTCATGTATCTTACACAGTCAACCTCTACAGAGTGTCTCATCTCTGGCTTTCATC	480			
Db 421	GCAGTCATGTATCTTACACAGTCAACCTCTACAGAGTGTCTCATCTCTGGCTTTCATC	480			
QY 481	AGTCTGGACCCGCTACTGTGGCCATGCTCCACGCGCACCAACAGTCAAGGCCAAGAACTG	540			
Db 481	AGTCTGGACCCGCTACTGTGGCCATGCTCCACGCGCACCAACAGTCAAGGCCAAGAACTG	540			
QY 541	TTGGCTGAAAAGTGATGTATGTTGGCTGTGGATCCCTGGCTCTGTGACTATATCC	600			
Db 541	TTGGCTGAAAAGTGATGTATGTTGGCTGTGGATCCCTGGCTCTGTGACTATATCC	600			
QY 601	GACTTCATCTTGGCCACGTCAGTGAAGGACAGATGACAGATATATCTGTGACCGCTTAC	660			
Db 601	GACTTCATCTTGGCCACGTCAGTGAAGGACAGATGACAGATATATCTGTGACCGCTTAC	660			
QY 661	CCCATGACTGTGGGT	720			
Db 661	CCCATGACTGTGGGT	720			
QY 721	CTGTGATTTGATCTCTGTCTCTGCTATTGCAATTAATCATCTCCAAAGCTGTCAACTCAAG	780			
Db 721	CTGTGATTTGATCTCTCTGCTATTGCAATTAATCATCTCCAAAGCTGTCAACTCAAG	780			
QY 781	GGCAGCAGGAAGGCGAAGGCGCTCAAGACACAGATCATCTCATCTGTGGCTTCTTGGC	840			
Db 781	GGCAGCAGGAAGGCGAAGGCGCTCAAGACACAGATCATCTCATCTGTGGCTTCTTGGC	840			
QY 841	TGTGGCGCCTTACTACATTTGGATGGATAGCATGCACTGCTTCATCTCTCTGGAAATCATC	900			

Db	841	TTGTTGGCGCCTTACTACATTTGGGATCAGCATCGACTCCTTATCCTCTCTGGAAATCATC	900
QY	901	AAGCAAGGGTGTAGTTGAGAAACCTGTGCACAACTGSAATTTCCATCACGAGGCCCTA	960
Db	901	AAGCAAGGGTGTGAGTTGGAACACCTGTGCACAACTGSAATTTCCATCACGAGGCCCTA	960
QY	961	GCTTCTTCCACTGATCTGTGCAACCCCATCCTATGCTTCTCTGGAGCCAAATTTAA	1020
Db	961	GCTTCTTCCACTGTGTCTGGAACCCCATCCTATGCTTCTCTGGAGCCAAATTTAA	1020
QY	1021	ACCTCTGCCAGCAGCAGCTACCTCTGTGAGCAGAGGGTCCAGCCTCAAGTCTCTCC	1080
Db	1021	ACCTCTGCCAGCAGCAGCTACCTCTGTGAGCAGAGGGTCCAGCCTCAAGTCTCTCC	1080
QY	1081	AAAGGAAAGCGAGGTGGACATTCATCTGTTCCACTGSAATCTGAGTCTTCAAGTTTCAAC	1140
Db	1081	AAAGGAAAGCGAGGTGGACATTCATCTGTTCCACTGSAATCTGAGTCTTCAAGTTTAC	1140
QY	1141	TCGACGTAAACAGANTAAAGAACTTTTTTTATACATAATAACTTTTTTAAGT	1200
Db	1141	TCGACGTAAACAGANTAAAGAACTTTTTTTATACATAATAACTTTTTTAAGT	1200
QY	1201	ACACATTTTTCAGATATATAAAGCTGACCAATATGTTACAGTTTTTATGCTTGTGAT	1260
Db	1201	ACACATTTTTCAGATATATAAAGCACTACCAATATGTTACAGTTTTTATGCTTGTGAT	1260
QY	1261	TTTGTCTGTGTTCTTTAGTTTGTGAGTTTAATGACTTATATATAAATTTT	1320
Db	1261	TTTGTCTGTGTTCTTTAGTTTGTGAGTTTAATGACTTATATATAAATTTT	1320
QY	1321	TTTGTTCATATTGATGTGTCTAGGCAAGGACTGTGAGTCTTGTGCTGTAT	1380
Db	1321	TTTGTTCATATTGATGTGTCTAGGCAAGGACTGTGAGTCTTGTGCTGTAT	1380
QY	1381	GTCCTGTGTGAGACTGTAAAAAAAGGAACTGAACATTCCTCAAGCGTGTAGTGAATCAG	1440
Db	1381	GTCCTGTGTGAGACTGTAAAAAAAGGAACTGAACATTCCTCAAGCGTGTAGTGAATCAG	1440
QY	1441	TAAAGCTAGAAATGATCCGAGCTGTTTATGCATATATCTCTCCATCCCGTGGAAAC	1500
Db	1441	TAAAGCTAGAAATGATATGCCAGCTGTTTATGCATATATCTCTCCATCCCGTGGAAAC	1500
QY	1501	GTTTTTCTGTCTTTAAGACGTATTTTGCCTGTAGAAATGCGACTATATACCAAGCCC	1560
Db	1501	GTTTTTCTGTCTTTAAGACGTATTTTGCCTGTAGAAATGCGACTTATTAACCAAGCCC	1560
QY	1561	AAAGGATATAGAAATGCTGTTTTTCAGTTTTACAGATGAGTGGTGTATTCACGACCTAC	1620
Db	1561	AAAGTGGATAGAAATGCTGTTTTTCAGTTTTACAGATGAGTGGTGTATTCACGACCTAC	1620
QY	1621	AGGTACAGTCTGTATTAAAGTTGTTAATAAAGTATCATGTATTAACCTTAAAAAATAAA	1680
Db	1621	AGGTACAGTCTGTATTAAAGTTGTTAATAAAGTATCATGTATTAACCTTAAAAAATAAA	1680
QY	1681	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCAGCAGACACTGGAATTC	1737
Db	1681	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCAGCAGACACTGGAATTC	1737
RESULT	3		
	US-08-701-265-3		
	Sequence 3, Application US/08701265		
	Patent No. 5776457		
	GENERAL INFORMATION:		
	APPLICANT: Chuntharapai, Anan		
	APPLICANT: <u>Lee, James</u>		
	APPLICANT: Hebert, Caroline		
	APPLICANT: Jin Kim, K.		
	TITLE OF INVENTION: Antibodies to Human P74A Receptors		
	NUMBER OF SEQUENCES: 6		
	CORRESPONDENCE ADDRESS:		
	ADDRESSEE: Genentech, Inc.		

STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Minipath (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/701,265
 FILING DATE: 22-AUG-1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/076093
 FILING DATE: 11-Jun-1993
 APPLICATION NUMBER: 07/810782
 FILING DATE: 19-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/677211
 FILING DATE: 29-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B
 REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: 706P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-5530
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1737 nucleotides
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 US-08-701-265-3

Query Match 100.0%; Score 1737; DB 3; Length 1737;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1737; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAATTCAGTGTGCTGGCGGCGGCGCAAGTGAAGCGCGGCGCTGAGTGTCCAGTA 60
 1 GAATTCAGTGTGCTGGCGGCGGCGGCGCAAGTGAAGCGCGGCGCTGAGTGTCCAGTA 60
 61 GCCACCGCATCTGGAGAACCAAGCGGTACCATGAGAGGGATCAGTATATACACTTCAGAT 120
 61 GCCACCGCATCTGGAGAACCAAGCGGTACCATGAGAGGGATCAGTATATACACTTCAGAT 120
 121 AACTACCGAGAGAAATGGGCTCAGGGGACTATGACTCCATGAAGAACCCGTTCCT 180
 121 AACTACCGAGAGAAATGGGCTCAGGGGACTATGACTCCATGAAGAACCCGTTCCT 180
 181 GAAGAAATGCAATTTCAATAAAATCTTCTGCCACCATCATCTCAATCTTCTTA 240
 181 GAAGAAATGCAATTTCAATAAAATCTTCTGCCACCATCATCTCAATCTTCTTA 240
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 421 GCAGTCATGTCTATACACAGTCAACCTCTACAGCAGTGTCTCATCTGCGCTTCATC 480
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421 GCAGTCATGTCTATACACAGTCAACCTCTACAGCAGTGTCTCATCTGCGCTTCATC 480
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 661 CCCAATGACTTGTGGGT 720
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 721 CCTGATATGTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
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 781 GGCACACGAAGCGGAGGCGCTCAAGACACAGTATCTCATCTGCTGCTGCTGCTGCTGCTGCT 840
 841 TTTTGGTGTGCTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 841 TTTTGGTGTGCTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 901 AAGCAAGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 901 AAGCAAGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
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 1021 ACCCTGCGCGACGACGACACTCCTCTGTGAGCAAGGCTCAGGCTCAAGTCTCTCC 1080
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 1081 AAGGAAAGCGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
 1141 TCCAGCTAACACAGATGTAAAGACTTTTATATAGATAAATACCTTTTAAAGT 1200
 1141 TCCAGCTAACACAGATGTAAAGACTTTTATATAGATAAATACCTTTTAAAGT 1200
 1201 ACACATTTTTCAGATATTAAGAACTGACCAATATGACAGTTTATGCTGTGGAT 1260
 1201 ACACATTTTTCAGATATTAAGAACTGACCAATATGACAGTTTATGCTGTGGAT 1260
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 1321 TTTTGTCTGTTCTTCTTATGTTTGTGAAGTTTAAATGACTTATATATATATATATTTT 1380
 1381 GTCCTGTGTAGACTGTAGAAAAGGAACTGAATTCAGAGGCTGTAGTGAATCAG 1440
 1381 GTCCTGTGTAGACTGTAGAAAAGGAACTGAATTCAGAGGCTGTAGTGAATCAG 1440
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 1441 TAAAGCTAAATGATATCCAGCTTTTATGATGATGATGATGATGATGATGATGATGATGAT 1500
 1501 GTTTTCTGTCTTAAAGCTGATTTTGTGTAGAGATGACCTTAAACCAAGGCC 1560
 1501 GTTTTCTGTCTTAAAGCTGATTTTGTGTAGAGATGACCTTAAACCAAGGCC 1560

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0Y 1561 AAAGTGTATAGAAATGCGTGTTTTCAGTATTTCAGAGAGTGGTGTATTTCAACACTAC 1620
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Db 1561 AAAGTGTATAGAAATGCGTGTTTTCAGTATTTCAGAGAGTGGTGTATTTCAACACTAC 1620
0Y 1621 AGTGTACATCTGTGTATAGTTGTATATAAGTACATGTTAACTTAAAAA 1680
    |||
Db 1621 AGTGTACATCTGTGTATAGTTGTATATAAGTACATGTTAACTTAAAAA 1680
0Y 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCGACGACACTGGAATTC 1737
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Db 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCCGACGACACTGGAATTC 1737

RESULT 4
US-08-284-586-3
; Sequence 3, Application US//08284586
; Patent No. 5840856
; GENERAL INFORMATION:
; APPLICANT: Chuntharapal, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PFAA Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284, 586
; FILING DATE:
;
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/076, 093A
; FILING DATE: 11-Jun-1993
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/577211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1737 nucleotides
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
;
US-08-284-586-3

Query Match 100.0%; Score 1737; DB 4; Length 1737;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1737; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
0Y 1 GAATTCAGTGTGCTGGCGCGCGGCAAGTGAACGCCGAGGCGCTGAGTCTCCAGTA 60
    1 GAATTCAGTGTGCTGGCGCGCGGCAAGTGAACGCCGAGGCGCTGAGTCTCCAGTA 60
    |||
Db 1 GAATTCAGTGTGCTGGCGCGCGGCAAGTGAACGCCGAGGCGCTGAGTCTCCAGTA 60
    |||

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QY	61	GCACCGCATCTGAGAGAACGACGGGTACCATTGAGGGGATCAGTATATATACCTTCAGAT	120
Db	61	GCCACCGCATCTGGAGAGAACGACGGGTACCATTGAGGGGATCAGTATATACCTTCAGAT	120
QY	121	AACCTACACCGAGGAAATGGGGCTCAGGGGACTATGATCCATGAAGAACCTCTTCCGT	180
Db	121	AACCTACACCGAGGAAATGGGGCTCAGGGGACTATGATCCATGAAGAACCTCTTCCGT	180
QY	181	GAAGAAAATGCTATTTTCATTAATAATTTTCCTCCACCACATGCTACGCCATCATTTCTTA	240
Db	181	GAAGAAAATGCTATTTTCATTAATAATTTTCCTCCACCACATGCTACGCCATCATTTCTTA	240
QY	241	ACTGGCATTTGGGGCAATGGATTGGTCATCTGGTCATGGGTTACCGAAGAAACTGAGA	300
Db	241	ACTGGCATTTGGGGCAATGGATTGGTCATCTGGTCATGGGTTACCGAAGAAACTGAGA	300
QY	301	AGCATGACGGACAGTACAGGCTGACACTGTCAAGTGTGGCGGACCTCCTCTTGTCACTACG	360
Db	301	AGCATGACGGACAGTACAGGCTGACACTGTCAAGTGTGGCGGACCTCCTCTTGTCACTACG	360
QY	361	CTTCCCTCTGGGCAAGTGTGATGCCGTGGCAAACTGGTACTTTGGGAACTTCCATATACAG	420
Db	361	CTTCCCTCTGGGCAAGTGTGATGCCGTGGCAAACTGGTACTTTGGGAACTTCCATATACAG	420
QY	421	GCAGTCATGTCACTACACAGTCAACCTCTACAGCAGTGTCCCTATCCTGGCCCTTCATC	480
Db	421	GCAGTCATGTCACTACACAGTCAACCTCTACAGCAGTGTCCCTATCCTGGCCCTTCATC	480
QY	481	AGTCGAGCGGCTACCTGGGCATCTGTCCACAGCCCAAGTCAAGGTCAGAGGCAAGGAAGCTG	540
Db	481	AGTCGAGCGGCTACCTGGGCATCTGTCCACAGCCCAAGTCAAGGTCAGAGGCAAGGAAGCTG	540
QY	541	TTGGCTGAAGAGTGTCTATGTTGGGCGTGTGATCCCTGCCCTCTGTGCTACTATCCC	600
Db	541	TTGGCTGAAGAGTGTCTATGTTGGGCGTGTGATCCCTGCCCTCTGTGCTACTATCCC	600
QY	601	GACTTCATCTTTGCCAAGCTGACTGAGGACGATGACAGATATATCTGTGACCGCTTCAC	660
Db	601	GACTTCATCTTTGCCAAGCTGACTGAGGACGATGACAGATATATCTGTGACCGCTTCAC	660
QY	661	CCCAATGACTGTGGGGGTGTGGTTCACATTTGACACATCATGTTGGGCTTATCCGTG	720
Db	661	CCCAATGACTGTGGGGGTGTGGTTCACATTTGACACATCATGTTGGGCTTATCCGTG	720
QY	721	CGTGATATGTCACTCCTGCTCCTATATTGATATATCTCCAAAGTGTCACTACATCCAAAG	780
Db	721	CGTGATATGTCACTCCTGCTCCTATATTGATATATCTCCAAAGTGTCACTACATCCAAAG	780
QY	781	GGCCACGAGAAGGCGACGCCCTCAAGACACACAGTCATCCTCTGGCTTTCTGGCC	840
Db	781	GGCCACGAGAAGGCGACGCCCTCAAGACACACAGTCATCCTCTGGCTTTCTGGCC	840
QY	841	TGTTGGCGCCTTCTCATATTGGGATCAGATGCACTCCTCATCTCCTCTGGAATTCATC	900
Db	841	TGTTGGCGCCTTCTCATATTGGGATCAGATGCACTCCTCATCTCCTCTGGAATTCATC	900
QY	901	AAGCAAGGGGTGTGATTGTGAACACTGTGCACAATGTGATTTTCATACCCAGGCCCTTA	960
Db	901	AAGCAAGGGGTGTGATTGTGAACACTGTGCACAATGTGATTTTCATACCCAGGCCCTTA	960
QY	961	GCTTTCTTCACACTGTCTGTGAAACCCCATCCTCATGCTTTCTTGGAGCCAAATTTTAAA	1020
Db	961	GCTTTCTTCACACTGTCTGTGAAACCCCATCCTCATGCTTTCTTGGAGCCAAATTTTAAA	1020
QY	1021	ACCTGTGCGCAGACGACATCACCCTCTGGAGAGAGGGTTCAGGCTCAAGAATCCTCTCC	1080
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QY	1081	AAAGAAAGCGAGGTGACATTCATCTGTTTCCACATGATCTGAGATCTTCAAGTTTTCAC	1140
Db	1081	AAAGAAAGCGAGGTGACATTCATCTGTTTCCACATGATCTGAGATCTTCAAGTTTTCAC	1140

QY	721	CGGGATTGTCATCCGTCCTCGTATGTGATATCATCTCCAAAGCTGTCACTCCAAAG	780
Db	721	CCTGGATTGTCATCTCTCTCTGATTTGATATATCATCTCCAAAGCTGTCACTCCAAAG	780
QY	781	GGCCACGAAAGCCCAAGGCCCTCAAGACCACAGTCATCCCTCATCTTGGCTTTCTTGCC	840
Db	781	GGCCACGAAAGCCCAAGGCCCTCAAGACCACAGTCATCTCTCATCTTGGCTTTCTTGCC	840
QY	841	TGTTGGCTGCTTACTACATTTGGGATAGCATGACTCTTCACTCTCTCTGGAATTCATC	900
Db	841	TGTTGGCTGCTTACTACATTTGGGATAGCATGACTCTTCACTCTCTCTGGAATTCATC	900
QY	901	AAGCAAGGCTGTGATTTGGAACACTGTGCACAAAGGATTTCCATTCACGAGAGCCCTA	960
Db	901	AAGCAAGGCTGTGATTTGGAACACTGTGCACAAAGGATTTCCATTCACGAGAGCCCTA	960
QY	961	GCTTTCTTCCACTGTGTCTGAACCCCATCTCTATGTTCTCTTGAGCCAAATTTAA	1020
Db	961	GCTTTCTTCCACTGTGTCTGAACCCCATCTCTATGTTCTCTTGAGCCAAATTTAA	1020
QY	1021	ACCTTGCCCGACGACGACCTACCTGTGAGAGAGGGCCAGCCTCAAGTCCCTGCC	1080
Db	1021	ACCTTGCCCGACGACGACCTACCTGTGAGAGAGGGCCAGCCTCAAGTCCCTGCC	1080
QY	1081	AAAGAAAGCGAGGTGACATTCATCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCAC	1140
Db	1081	AAAGAAAGCGAGGTGACATTCATCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCAC	1140
QY	1141	TCCAGCTACACACATGTAAAGACCTTTTTTTATACGATTAATAACTTTTTTAAAGTT	1200
Db	1141	TCCAGCTACACACATGTAAAGACCTTTTTTTATACGATTAATAACTTTTTTAAAGTT	1200
QY	1201	ACACATTTTTCAGATATAAAGACTGACCAATATGTACAGTTTATAGCTTGCTGGAT	1260
Db	1201	ACACATTTTTCAGATATAAAGACTGACCAATATGTACAGTTTATAGCTTGCTGGAT	1260
QY	1261	TTTTGCTGTGTTCTTTAGTTTGTGCAAGTTTAATGACTATTTATATATAATTTTT	1320
Db	1261	TTTTGCTGTGTTCTTTAGTTTGTGCAAGTTTAATGACTATTTATATATAATTTTT	1320
QY	1321	TTTGTTCATATTGATGTGTGTACGACGACCTGTGGCCAAAGTTTATGTTGCTGAT	1380
Db	1321	TTTGTTCATATTGATGTGTGTACGACGACCTGTGGCCAAAGTTTATGTTGCTGAT	1380
QY	1381	GTCCTGTGTAGGACTGTAGAAAAGGAACTGAACATTCACAGCGGTAGTGAATCACG	1440
Db	1381	GTCCTGTGTAGGACTGTAGAAAAGGAACTGAACATTCACAGCGGTAGTGAATCACG	1440
QY	1441	TAAAGCTAGAATGATGCCAGCTGTTTATGCATAGATATCTTCCATTCCTCGTGAAAC	1500
Db	1441	TAAAGCTAGAATGATGCCAGCTGTTTATGCATAGATATCTTCCATTCCTCGTGAAAC	1500
QY	1501	GTTTTTCCTGTTTAAAGACGATTTTCTGTAGAAAGTGCACATTAAACCAAAGGCC	1560
Db	1501	GTTTTTCCTGTTTAAAGACGATTTTCTGTAGAAAGTGCACATTAAACCAAAGGCC	1560
QY	1561	AAATGCTATAGAAATGCTGTGTTTTCAGTTTCAGAGATGGGTGATTTACAGACCTAC	1620
Db	1561	AAATGCTATAGAAATGCTGTGTTTTCAGTTTTCAGAGATGGGTGATTTACAGACCTAC	1620
QY	1621	AGTGTACGCTGTATTAAGTTGTTAAATAAAGTGCATGTTAACTTAAAAA	1680
Db	1621	AGTGTACGCTGTATTAAGTTGTTAAATAAAGTGCATGTTAACTTAAAAA	1680
QY	1681	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCCGACGACACTGGAATTC	1737
Db	1681	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCCGACGACACTGGAATTC	1737

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1 APPLICANT: Chuntharapel, Anan
2 APPLICANT: Lee, James
3 APPLICANT: Hebert, Caroline
4 APPLICANT: K. Jin Kim
5 APPLICANT: Genentech, Inc.
6 TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY DISORDERS
7 NUMBER OF SEQUENCES: 3
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Genentech, Inc.
10 STREET: 460 Point San Bruno Blvd
11 CITY: South San Francisco
12 STATE: California
13 COUNTRY: USA
14 ZIP: 94080
15
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
18
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: palin (Genentech)
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: PCT/US94/06380
24 FILING DATE:
25
26 CLASSIFICATION:
27
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: 08/076093
30 FILING DATE: 11-JUN-1993
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Love, Richard B.
33 REGISTRATION NUMBER: 34,659
34 REFERENCE/DOCKET NUMBER: 706P2P1
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: 415/225-5530
37 TELEFAX: 415/952-9881
38 TELEX: 910/371-7168
39 INFORMATION FOR SEQ ID NO: 2:
40
41 SEQUENCE CHARACTERISTICS:
42
43 LENGTH: 1737 bases
44 TYPE: nucleic acid
45 STRANDEDNESS: single
46 TOPOLOGY: linear
47
48 PCT-US94-06380-2
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Db 361 CTTCCTTCCTGGGAGTTGATGCCGCGGCAACTGCTACTTTGGGAACTTCTCATGCAAG 420
OY 421 GCAGTCATATGTATCTACACAGTCAACCTCTACAGCAGTGTCTCTACTCTGGCCTTCATC 480
Db 421 GGAGTCATATGTATCTACACAGTCAACCTCTACAGCAGTGTCTCTACTCTGGCCTTCATC 480
OY 481 ACTCTGAGCAGGCTACCTGGCCATCGTCGACGACGACCAAGCAGTCAAGGCAAGAAAGCTG 540
Db 481 ACTCTGAGCAGGCTACCTGGCCATCGTCGACGACGACCAAGCAGTCAAGGCAAGAAAGCTG 540
OY 541 TTGGCTGAAGAGGTGGTCTATGTGGCGCTGTGATCCCTGCCCCCTGCTGATCTATCC 600
Db 541 TTGGCTGAAGAGGTGGTCTATGTGGCGCTGTGATCCCTGCCCCCTGCTGATCTATCC 600
OY 601 GACTTCATCTTTGGCCAGCTCAGTGAAGCAGATGACAGATATATCTGTACCGCTTCTAC 660
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Db 661 CCCAATGACTTGTGGGTGGTGTGTCAGATTTCAGACATCATAGSTTGGCCTTATCTG 720
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Db 781 GGGCAGCAAGACGCGAAGGCGCTCAAGACAGATATCTCTGCTGCTTCTTCTGCGC 840
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Db 901 AAGCAAGGGGTGTGAGTTTGAAGACACTGTGCACAAAGTGATTTCCATCCAGGCGCTTA 960
OY 961 GCTTTCTTCCACTGTGTGTGAACCCCATCTCTATGCTTCTTGGAGCCAAATTTAA 1020
Db 961 GCTTTCTTCCACTGTGTGTGAACCCCATCTCTATGCTTCTTGGAGCCAAATTTAA 1020
OY 1021 ACCTTGCCGACGACGACACTCAGCTGTGAGAGAGAGGGTCCAGCTCAAGATCTCTCC 1080
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OY 1081 AAAGAAAGCGAGGTGACATTCATCTGTTCCACTGAGTCTGAGTCTTCAAGTTTCA 1140
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OY 1141 TCCAGCTACAGAGATTAAGACCTTTTATACGATTAATACTTTTATTAAGT 1200
Db 1141 TCCAGCTACAGAGATTAAGACCTTTTATACGATTAATACTTTTATTAAGT 1200
OY 1201 ACACATTTTTCAGATTAAGAACTGACCAATTTTACAGTTTATGCTGTGGAT 1260
Db 1201 ACACATTTTTCAGATTAAGAACTGACCAATTTTACAGTTTATGCTGTGGAT 1260
OY 1261 TTTTGTCTGTCTTCTTATGTTTGTGAAGTTTATGACTTATTAATAATTTT 1320
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Db 1321 TTTGTTTATATGATGTGTCTAGGCAAGGACCTGTGGCAAGTTCTAGTGTGAT 1380
OY 1381 GTCTGCTGATAGAGCTGTGAAGAAAGGAACTGAACATTCAGAGCTGTAGTGAATCAG 1440
Db 1381 GTCTGCTGATAGAGCTGTGAAGAAAGGAACTGAACATTCAGAGCTGTAGTGAATCAG 1440
OY 1441 TAAAGCTAGAAATGATCCGAGCTGTTATGATAGATATATCTCCATCCCGTGAAC 1500
Db 1441 TAAAGCTAGAAATGATCCGAGCTGTTATGATAGATATATCTCCATCCCGTGAAC 1500

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OY 1501 GTTTTCCTGTCTTAAACGCTGATTTGCTGTAGAGATGGCACTTATTAACCAAGCCC 1560
Db 1501 GTTTTCCTGTCTTAAACGCTGATTTGCTGTAGAGATGGCACTTATTAACCAAGCCC 1560
OY 1561 AAAGTGTATAGAAATGCTGTTTTCAGTTTTCAGAGTGGGTGATTTACGACCTAC 1620
Db 1561 AAAGTGTATAGAAATGCTGTTTTCAGTTTTCAGAGTGGGTGATTTACGACCTAC 1620
OY 1621 AGTGTACAGCTCTGTATTAAGTTGTTAATAAGTACATGTTAACTTAAAAA 1680
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OY 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1737
Db 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1737

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RESULT 7

US-08-153-848-45

; Sequence 45, Application US/08153848

; Patent No. 5759804

; GENERAL INFORMATION:

; APPLICANT: Godiska, Ronald

; APPLICANT: Gray, Patrick W.

; APPLICANT: Schweikert, Vicki L.

; TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/153,848

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/977,452

; FILING DATE: 17-NOV-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5759804e1, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 31794

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 474-6300

; TELEFAX: (312) 474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 45:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1317 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: CDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 201..1211

; US-08-153-848-45

Query Match 64.4%, Score 1118.2, DB 3, Length 1317,
 Best Local Similarity 99.6%, Pred. No. 1.5e-224;
 Matches 1131; Conservative 0; Mismatches 3; Indels 1; Gaps 1.

106 ATATACACTTCAGATTAACACCGAGAAATGGGCTCAGGGGACTATGACTCCATGAAG 165
171 ATATACACTTCAGATTAACACCGAGAAATGGGCTCAGGGGACTATGACTCCATGAAG 230
166 GAACCCCTGTTCCGTCGAGAAATGCTAATTTCAATAAATCTCTGCGCCACCATCTAC 225
231 GAACCCCTGTTCCGTCGAGAAATGCTAATTTCAATAAATCTCTGCGCCACCATCTAC 290
226 TCATCATCTTTCTTAAGTCGATTTGGGCAATGATTTGTCATCTCTGTCATGGGTTAC 285
291 TCATCATCTTTCTTAAGTCGATTTGGGCAATGATTTGTCATCTCTGTCATGGGTTAC 350
286 CAGAAGAACTGAGAAGCATGAGCGAGATGACAGGCTCAGCTGTCATGGGCGGCTAC 345
351 CAGAAGAACTGAGAAGCATGAGCGAGATGACAGGCTCAGCTGTCATGGGCGGCTAC 410
346 CTCCTTTGTCATCAGGCTTCCCTCTGCGGAGTTGATGCCGTCGCAAACTGTCATTTGGG 405
411 CTCCTTTGTCATCAGGCTTCCCTCTGCGGAGTTGATGCCGTCGCAAACTGTCATTTGGG 470
406 AACTTCCTTATGAGAAGCATGATGATCTACACAGTCAACCTCTACAGCATGTCCTC 465
471 AACTTCCTTATGAGAAGCATGATGATCTACACAGTCAACCTCTACAGCATGTCCTC 530
466 ATCTGACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 525
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526 AGGCCAAGAACTGTTGGCTGAAAAAGTGTATGTTGGGCTGATGATGATGATGATGATGAT 585
591 AGGCCAAGAACTGTTGGCTGAAAAAGTGTATGTTGGGCTGATGATGATGATGATGATGAT 650
586 CTGCTGACATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 645
651 CTGCTGACATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 710
646 TGTGACCGCTTACCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 705
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706 GTTGGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 765
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766 CTGTACACATTCGAGGCGCCAGCAAGGCGCTCAAGACCAACATCCTCCGCTAC 825
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946 ATCACCAGAGGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1005
1011 ATCACCAGAGGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1070
1006 GGAGCCAAATTTAAACCTGCGCCAGCAGCAGTCACTCTGTGAGCAGAGAGGCTCCAGC 1065
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1066 CTCAGATTCCTGCAAGAGAAAGGAGGTGACATTCATCTGTTCCACTGAGTCTGAG 1125
1131 CTCAGATTCCTGCAAGAGAAAGGAGGTGACATTCATCTGTTCCACTGAGTCTGAG 1190
1126 TCTTCAAGTTTCACTCCAGCTAACACAGATGTAAAGACTTTTATTTATAGATAAATA 1185
1191 TCTTCAAGTTTCACTCCAGCTAACACAGATGTAAAGACTTTTATTTATAGATAAATA 1249
1186 ACTTTTATTTAAGTTACACATTTTTCAGATATTAAGAGACTGACCAATATTTGACA 1240

Db 1250 ACCTTTATTTAAGTTACACATTTTTCAGATATTAAGAGACTGACCAATATTTGAAAA 1304

RESULT 8
PCT-US93-11153-45
Sequence 45, Application PC/TUS9311153
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schelkard, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 201..1211
PCT-US93-11153-45

Query Match 64.4%; Score 118.2; DB 5; Length 1317;
Best Local Similarity 99.6%; Pred. No. 1.5e-224;
Matches 1131; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Db 106 ATATACACTTCAGATTAACACCGAGAAATGGGCTCAGGGGACTATGACTCCATGAAG 165
171 ATATACACTTCAGATTAACACCGAGAAATGGGCTCAGGGGACTATGACTCCATGAAG 230
166 GAACCCCTGTTCCGTCGAGAAATGCTAATTTCAATAAATCTCTGCGCCACCATCTAC 225
231 GAACCCCTGTTCCGTCGAGAAATGCTAATTTCAATAAATCTCTGCGCCACCATCTAC 290
226 TCATCATCTTTCTTAAGTCGATTTGGGCAATGATTTGTCATCTCTGTCATGGGTTAC 285
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286 CAGAAGAACTGAGAAGCATGAGCGAGATGACAGGCTCAGCTGTCATGGGCGGCTAC 345
351 CAGAAGAACTGAGAAGCATGAGCGAGATGACAGGCTCAGCTGTCATGGGCGGCTAC 410

Qy	346	CTTTTGTCATCAAGCTTCCTCCTTCGGGAGTTGATGCCGTGGCAAACTGGTACTTGGG	405
Db	411	CTCTTTGTCATCAAGCTTCCTCCTTCGGGAGTTGATGCCGTGGCAAACTGGTACTTGGG	470
Qy	406	AAC TTCCTATGACAGGACGATCATGTCTATCTACAGATCAACCTCTACAGCAGTGTCTC	465
Db	471	AAC TTCCTATGACAGGACGATCATGTCTATCTACAGATCAACCTCTACAGCAGTGTCTC	530
Qy	466	ATCTGGCCTTCATCAAGCTTCGGGAGCTTCAGCTGATGTCACAGGACCAACAGTCAG	525
Db	531	ATCTGGCCTTCATCAAGCTTCGGGAGCTTCAGCTGATGTCACAGGACCAACAGTCAG	590
Qy	526	AGGCGAAGAAAGCTGTGGCTGAAAAGGTGATCTATGTGGGCGTCGATCCCTGCCCTC	585
Db	591	AGGCGAAGAAAGCTGTGGCTGAAAAGGTGATCTATGTGGGCGTCGATCCCTGCCCTC	650
Qy	586	CTGCTGACTATCCCGACTTCATCTTTGCCACGTCAGTCGAGGACGATGACGATATATC	645
Db	651	CTGCTGACTATCCCGACTTCATCTTTGCCACGTCAGTCGAGGACGATGACGATATATC	710
Qy	646	TGTACCGCTTACACCCCATGACTGTGGGCTGTGTCTTCACATTCAGACATCATG	705
Db	711	TGTACCGCTTACACCCCATGACTGTGGGCTGTGTCTTCACATTCAGACATCATG	770
Qy	706	GTTGGCCTTATCCTGCTGTGATTTGTATCTGTCTCTATTTGATTTATCATCTCCAG	765
Db	771	GTTGGCCTTATCCTGCTGTGATTTGTATCTGTCTCTATTTGATTTATCATCTCCAG	830
Qy	766	CTGTACACATCCAAAGGGCCACCAAGAGCGCAAGGCCCTCAAGCCACAGTCATCTCATC	825
Db	831	CTGTACACATCCAAAGGGCCACCAAGAGCGCAAGGCCCTCAAGCCACAGTCATCTCATC	890
Qy	826	CTGGCTTCTTCGCGCTGTTGGCTGCTTACTACATTTGGATGAGATGACTCTCTTCATC	885
Db	891	CTGGCTTCTTCGCGCTGTTGGCTGCTTACTACATTTGGATGAGATGACTCTCTTCATC	950
Qy	886	CTCTCGGAATCATCAAGCAAGGCTGTGAATTTGAAACACATGTGACAAAGTGGATTCC	945
Db	951	CTCTCGGAATCATCAAGCAAGGCTGTGAATTTGAAACACATGTGACAAAGTGGATTCC	1010
Qy	946	ATCACCGAGGCTCAGCTTTCTTCACATGTGTCTCAACCCCATCCTCATCTCTTCCTT	1005
Db	1011	ATCACCGAGGCTCAGCTTTCTTCACATGTGTCTCAACCCCATCCTCATCTCTTCCTT	1070
Qy	1006	GGAGCCAAATTTAAACCTCTGCCACACGCACTACTCTGTGACGAGAGGTTCCACG	1065
Db	1071	GGAGCCAAATTTAAACCTCTGCCACACGCACTACTCTGTGACGAGAGGTTCCACG	1130
Qy	1066	CTCAAGATCTCTCCAAAGGAAACGAGGTGGACATTCATCTGTCCACTGAGTCTGAG	1125
Db	1131	CTCAAGATCTCTCCAAAGGAAACGAGGTGGACATTCATCTGTCCACTGAGTCTGAG	1190
Qy	1126	TCTTCAGATTTCTACCTCAGCTACACAGATGTAAAAAGACTTTTTTTATACGATAAATA	1185
Db	1191	TCTTCAGATTTCTACCTCAGCTACACAGATGTAAAAAGACTTTTTTTATACGATAAATA	1245
Qy	1186	ACTTTTTTTAAAGTATACATTTTTCAGATATATAAAGACAGACCATATTGATACA	1240
Db	1250	ACTTTTTTTAAAGTATACATTTTTCAGATATATAAAGACAGACCATATTGATAAA	1304

Sequence 3, Application PC/TUS9503032
GENERAL INFORMATION:
APPLICANT: Repigen Corporation
APPLICANT: the Trustees of Boston University
TITLE OF INVENTION: ANTIBODIES TO INTERLEUKIN-8 RECEPTORS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03032
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/237,937
FILING DATE: 02-MAY-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/210,250
FILING DATE: 15-MAR-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,842
FILING DATE: 09-DEC-91
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/726,606
FILING DATE: 09-JUL-91
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/685,101
FILING DATE: 10-APR-91
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04/66/015WO1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1373
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-03032-3

Query Match 11.6%; Score 201.2; DB 5; Length 1373;
Best Local Similarity 54.8%; Pred. No. 11e-33;
Matches 467; Conservative 0; Mismatches 373; Indels 12; Gaps 3;

QY 175 TTCGGTGAAGAAATGCTAATTTCAATAAAATCTCTGCGCCACGATCACTGCATC 234
DB 179 TGCCTGAGAAATCTGTGAAACCAACAGCTATGTGTCTATCACTATATCTGTC 238
QY 235 TTCTTACTGCGATTTGGGCAATGATGTGTCATCTGTCTATGCGTTACCAAGAA 294
DB 239 TTCTGCTGCTGCTGCTGCGCACTCCCTGCTGATCTGTCTATCTGTACACCGG 298
QY 295 CTGAGACGATGAGGCAAGTACGAGTGCAGCTGCAGTGGCGACCGCTCTTGTG 354
DB 299 ACCTGCTGCTGACGACGCTACCTGCTGAACTGCGCATCGCCGACCTGCTTGGCC 358
QY 355 ATCAGCTTCCTTCTGGGCGAGTTGATGCGGTGGCAAACTGTACTTTGGGAACTCT 414

DB 359 ACCACTTGGCCATCTGCGCCGCTCCCAAGGTGACAGCGGTGATCTTGGACAGCCCTG 418
QY 415 TGCAGGAGTCATGCTGATCATACAGTCAACCTCTACAGAGTGTCTCATCTGCGC 474
DB 419 TGTAAAGTGTCTGCTTGTGAAGAACTCACTTCTACAGCGAATCTGCTCTGSCC 478
QY 475 TTCTATGCTGTGAGCGGTACTGTGCGCATGTCACGCGACCAACAGTCAAGAGGCAAG 534
DB 479 TGCATCAGTGTGAGCGGTACTGTGCGCATGTCACGCGACCAACAGTCAAGAGG 538
QY 535 AAGCTGTGCTGAAAGAGTGTATGTGCGCTGTGATCTGCGCTCTGCTGACT 594
DB 539 CGCCACTTGT--GTCAAGTCAATATGCTTAAGCAAGTGGGAGTGTCTTGTACTGCT 595
QY 595 ATTCCGACTTCATCTTGTCCCAAGCTGAGTGAAGCA--GATGACAGATATATCTG-- 648
DB 596 CTGCGCATCTTACTTTCGATATGCAATCTTCCACCAATTCAGCGCGGTCTGCTAT 655
QY 648 --TGACCGCTTCTACCCCAATGACTTGTGGTGTGTGTTCAGATTTCAGACATCATG 705
DB 656 GAGGACATGGGAGACAGCACTGCGAAATGGCGCATGTGCTGCGGATCTGCTCAGACT 715
QY 706 GTTGCCTTATCTGCTGCTGATGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 765
DB 716 TTGGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 775
QY 766 CTGTCACTCTCAAGGCGCACAGAGGCAAGGCGCCCTCAAGACAGATCATCTCATC 825
DB 776 CTGTTCCAGGCGCCACATGGGCGAGAGCAAGGCGCATGCGGCTATCTTCCCTGCTG 835
QY 826 CTGGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 885
DB 836 CTGATCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 895
QY 886 CTCTCGAATATATCAAGCAAGGCTGTGATGTGAAACACTGTGCAAGTGTGATTC 945
DB 896 AGGACCCAGTGTATCAGAGAGCTGTGAGCGCGCAATGACATTCACCGGCGCTGAGC 955
QY 946 ATCAGCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1005
DB 956 GCCACGAGATCTGCGCTTCTGTCAGAGCTGCTGCAACCCCATATATCTAGCCTTCA 1015
QY 1006 GGAGCCAAATTT 1017
DB 1016 GGGCAAAAGTTT 1027

RESULT 12
PCT-US92-02977-1
Sequence 1, Application PC/TUS9202977
GENERAL INFORMATION:
APPLICANT: Navarro, Javier et al.
TITLE OF INVENTION: INTERLEUKIN-8 RECEPTORS AND
TITLE OF INVENTION: RELATED MOLECULES AND
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02977
FILING DATE: 19920410
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/685,101
 FILING DATE: April 10, 1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 00231/051002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200134
 INFORMATION FOR SEQ ID NO: 1
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1200
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 PCT-US92-02977-1

Query Match 11.5%; Score 200.4; DB 5; Length 1200;
 Best Local Similarity 54.5%; Pred. No. 1.5e-33;
 Matches 452; Conservative 0; Mismatches 366; Indels 12; Gaps 2;

QY 197 TCAATAAATCTCTGCCACACTACTATCTCTTAACCTGGATGGGCA 256
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 232 TTACAATAATGTTGTGCTCTCATCTATGCCGTGCTCTGCTGAGCCTGGGCA 291
 QY 257 ATGATTTGCTATCTGCTGCTATGGGTTACGAAAGAACTGAGAGCAATG 316
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 292 ACTCCCTGGTATGCTGCTACTGTAACGCGGAGCAACGTTGCTGCTACCACTGCT 351
 QY 317 ACAGGCTGCACCTGCTGATGCGGACCTCTCTTGTATCATCGGTTCCCTTGGGAG 376
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 352 ACCTGCTGAACCTGCGCATGCCACCTGCTTTTGGCCTACCATGCTTATGCGGCG 411
 QY 377 TTGATGCGGTGCAACTGCTACTTTGGAACTTCTATGCAAGCAAGTCCATCT 436
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 412 TCTCAAGAAAGAGCGTGAATTTGCGACGCGCCCTGTGCAAGTGGGCTGGTTGGA 471
 QY 437 ACAGAGTCAACCTCTACAGAGTCTCTCTATCTGCGCTTATAGTGTGAGCGCTACC 496
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 472 AGAAGTCAACTTCTAGTAAGTAAATCTGCTGCGCTGATGATGATGAGCGCTACC 531
 QY 497 TGGCATCTGTCACGCGCACCAACAGTACAGAGCGCAAGAACTGTGGCTGAAAGGTGG 556
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 532 TGGCATTTGCTCATGCTACTGTGACACTGACCCAGAGCGCACTTG---GTCAAGTTCA 588
 QY 557 TCTATGTTGGGCTGTGATCCCTGCTCTGCTGACTATTCGCACTTCAATCTTTGGCA 616
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 589 TATGCTGGGATCTGGGCGCTGCTGATTTTGGCTCCCTTCTCTCTTCTTCCGCC 648
 QY 617 ACCTGATGAGGCGAGTACAGCA-----TATATCTGAGCGCTTCTACCCCAATG 667
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 649 AAGTCTTTTCTCCAAACAATTCACGCCCGGTCTCTATGAGAGCTGGGTACACAACAG 708
 QY 668 ACTTGGGGTGTGTGTTTCAGTTTTCAGACATCATGTTGGCTTATCTGCTGGTGA 727
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 709 CGAATGGCGCATGCTGCGGATTCGCGCACACACTTTCGGTTACTCTGCGGCTGC 768
 QY 728 TTGTCATCTCTGCTGCTATTTGATTTATCATCTCCAAAGCTTCACTCCAAAGGCCAAC 787
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 769 TGGCATGCTGTTTGTATGGGTTACCCGCTGACGCGTTCAGAGCCCAACATGGGCG 828
 QY 788 AGAAGCGCAAGCCCTCAAGACACAGTATCTATCTGCTGGTTTTCGCTGGTGGC 847
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 829 AGAAGCACCGGGCATATGGGGTCTATCTTCCGCTGCTGCTATCTTCTTCTGCTGGC 888
 QY 848 TGCCTTACTACATTTGGATCGATCGACTCTCTTCTCTCTGAAATCATCAAGCAAG 907
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 889 TGGCTTCAACATGCTGCTGCTGCGACACACCTCATGAGACCAAGTGTCCAGGAGA 948
 QY 908 GGCTGAGTTTGAACACAGTGTGACAAAGTGTGATTTTCATCACCGAGCCCTTACTTCT 967
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 949 CGTGTCAAGCTCGCAATGACATTCACCGGGCCCTTGAGACCCACCGAGATTTCTGGGCTTCC 1008
 QY 968 TCCACTGTTGTGTGAACCCCATTCCTATGCTTCTTGGAGCCCAATTT 1017
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1009 TGCACAGCTGCTCAACCCCATCATCTACGCTTCAATTTGGCCAAACTTT 1058

RESULT 13
 US-08-202-056-2
 Sequence 2, Application US/08202056
 Patent No. 5440021
 GENERAL INFORMATION:
 APPLICANT: Chuntharapai, Anan
 APPLICANT: Hebert, Caroline
 APPLICANT: Kim, Kyung Jin
 APPLICANT: Lee, James
 TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/202,056

FILING DATE: 25-FEB-1994

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/677211

FILING DATE: 29-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: 706P3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5530

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1883 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-202-056-2

Query Match 11.3%; Score 196.8; DB 1; Length 1883;
 Best Local Similarity 53.9%; Pred. No. 9.8e-33;
 Matches 455; Conservative 0; Mismatches 377; Indels 12; Gaps 2;

QY 183 AGAAATGCTAATTTCAATAAATCTTCTGCCCCACCATCTACTCATCATCTTTTAAAC 242
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 96 AGAAATGAGACACTCAACAAAGTATGTTGATCATATGCTATGCTTATGTTCTGCT 155
 QY 243 TGGCATTTGGGGAATGAGTATGTCATCCCTGTCATGCGTTTACAGAAACTGAGAG 302
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 156 GAGCTCTGAGAACTCCCTGATGCTGCTGATCTTATTAACAGAGGCTCGGCGCTC 215
 QY 303 CATGACGACAAGTACAGAGCTGTCAGTGCAGCGGACCTCTCTTTGCTACAGCT 362
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 216 CGTACTGATGTCTACTGCTGAACTGGCCTTGGCGAGCTACTCTTTGCTGAGCTT 275
 QY 363 TCCCTTTGGGCAAGTGTATCCCTGCAAACTGTACTTTGGAACTTCTTAACAGGC 422
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 276 GCCCATCTGGGCGGCTCCAAAGGTGAATGCTGATTTTGGCAATCTCTGTCAGAGT 335

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 14, 1999, 09:52:22 : Search time 284.76 Seconds
(without alignments)
12032.205 Million cell updates/sec

Title: US-09-104-063-3

Perfect score: 1737
Sequence: 1 GAATTCAGTGTGCTGGCG.....CCGCAGACACTGGAATTC 1737

Scoring table: IDENTITY_NUC

Searched: 2546578 seqs, 986266752 residues

Database :

EST:*
1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
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50: em_est50:*
51: em_est51:*
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53: em_est53:*

54: em_est22:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	670.8	38.6	786	37	AA707668	AA707668 zj29f12.s
2	646.8	37.2	792	38	AA781110	AA781110 a123e10.s
3	606.6	34.9	693	36	AA634211	AA634211 ac72b06.s
4	601.4	34.6	657	47	AI493618	AI493618 th39e07.x
5	592.4	34.1	651	36	AA634201	AA634201 ac72b07.s
6	589	33.9	589	40	AA935648	AA935648 cp27c09.s
7	567.8	32.7	599	33	AA411265	AA411265 zv24f06.i
8	546.8	31.5	593	35	AA576017	AA576017 nm57d04.s
9	544.8	31.4	556	38	AA743645	AA743645 ny24g09.s
10	539	31.0	539	36	AA610463	AA610463 np97b09.s
11	514.6	29.6	521	34	AA479467	AA479467 zv17f10.r
12	511.8	29.5	555	38	AA747545	AA747545 nx85d08.s
13	506	29.1	583	29	AA148282	AA148282 zo45e12.s
14	501.2	28.9	536	38	AA804282	AA804282 mw30h06.s
15	501	28.8	501	33	AA426644	AA426644 zv47h11.s
16	492.2	28.3	524	44	AI249788	AI249788 qx51c10.x
17	491.4	28.3	509	38	AA760743	AA760743 n210b09.s
18	490.8	28.3	531	46	AI434652	AI434652 t134d02.x
19	485	27.9	504	43	AI159856	AI159856 qb51c09.x
20	483.4	27.8	535	41	AI022030	AI022030 cw72a11.x
21	473.8	27.3	524	48	AI583169	AI583169 tr98d12.x
22	470.6	27.1	538	39	AA824607	AA824607 cc83f08.s
23	470	27.1	470	33	AA426566	AA426566 zv47h11.r
24	464.6	26.7	473	44	AI300764	AI300764 qp50c09.x
25	462.8	26.6	482	41	AI002547	AI002547 cq90e01.s
26	458.2	26.4	483	45	AI344724	AI344724 qp04h09.x
27	456.8	26.3	552	37	AA731086	AA731086 rw68e05.x
28	448.6	25.8	455	44	AI300807	AI300807 qp47b03.s
29	446.8	25.7	537	34	AA479357	AA479357 zv17f10.s
30	439.4	25.3	456	32	AA354393	AA354393 EST52864
31	434.8	25.0	494	31	AA284569	AA284569 zt22e05.r
32	433.6	25.0	639	39	AA816049	AA816049 vr14h02.r
33	429.8	24.7	465	45	AI370816	AI370816 fa58c10.x
34	428	24.6	488	30	AA259199	AA259199 nc17b08.r
35	424.4	24.4	793	29	AA182270	AA182270 mt83f01.r
36	419	24.1	419	44	AI284206	AI284206 q126h07.x
37	416.4	24.0	475	43	AI193140	AI193140 qe40f12.s
38	415.4	23.9	417	45	AI358446	AI358446 qx19c11.x
39	415	23.9	454	31	AA284857	AA284857 zt22e05.s
40	413	23.8	437	50	AI675038	AI675038 wc22f10.x
41	409	23.5	409	34	AA490436	AA490436 aa51e04.r
42	404	23.3	405	50	AI682902	AI682902 wc69g07.x
43	401	23.1	401	49	AI660355	AI660355 we62b07.x
44	393.4	22.6	427	40	AA934663	AA934663 co71c08.s
45	393	22.6	393	33	AA386000	AA386000 EST99758

ALIGNMENTS

RESULT 1
AA707668/c 786 bp mRNA
LOCUS
DEFINITION zj29f12.s1 Soares fetal_liver-spleen_infls_S1 Homo sapiens cDNA
clone IMAGE:451727.3' similar to gb:L06797 PROBABLE G
PROTEIN-COUPLED RECEPTOR LCRI1 HOMOLOG (HUMAN);, mRNA sequence.
ACCESSION
AA707668
NTD g2717586


```

Db 621 GANAGAGGTCCAGACCTTCAGAGACCTCTCCAAAGGAAGCCAAAGTGACATTCATCTGT 562
Qy 1110 TTCACCTAGCTGAGTCTTCAAGTTTCACCCAGCTAACACAGATGAAAGACTTTT 1169
Db 561 TCCACGAGAGCTGAGTC-TCAAGGTTTCACCTCCAGCTAACACAGATGAAAGACTTTT 503
Qy 1170 TTTTATACGATAAATACCTTTTAAAGTACATTTTCAGATTAATAAAGACTGACC 1229
Db 502 TTTTATACGATAAATACCTTTTAAAGTACATTTTCAGATTAATAAAGACTGACC 443
Qy 1230 AATATTTGACAGTTTAAATGCTTTGGANTTTTGTCTGTCTTTTAACTTTTGTG 1289
Db 442 AATATTTGACAGTTTAAATGCTTTGGANTTTTGTCTGTCTTTTAACTTTTGTG 383
Qy 1290 AAGTTAATGCTAATTAATTAATTTTGTTCATATGAGTGCTAGGCA 1349
Db 382 AAGTTAATGCTAATTAATTAATTTTGTTCATATGAGTGCTAGGCA 323
Qy 1350 GGACCTGTGGCCAAAGTCTTAAAGTCTGATGCTGCTGAGAGCTAGAAAAGGGA 1409
Db 322 GGACCTGTGGCCAAAGTCTTAAAGTCTGATGCTGCTGAGAGCTAGAAAAGGGA 263
Qy 1410 CTGAACATTTCCAGAGCGTGTAGTGAATCACTAAAGCTAAGAAATATCCAGCTGTTTA 1469
Db 262 CTGAACATTTCCAGAGCGTGTAGTGAATCACTAAAGCTAAGAAATATCCAGCTGTTTA 203
Qy 1470 TGCATAGTAATCTCTCATTCCTCCGCTGGAAGCTTTTCTGTTTAAAGCTGANTTTG 1529
Db 202 TGCATAGTAATCTCTCATTCCTCCGCTGGAAGCTTTTCTGTTTAAAGCTGANTTTG 143
Qy 1530 CTGTAGAGATGAGCACTTATAACCAAGCCAAAGTGTATGAATAGTGTGTTTTCAG 1589
Db 142 CTGTAGAGATGAGCACTTATAACCAAGCCAAAGTGTATGAATAGTGTGTTTTCAG 83
Qy 1550 TTTTCAGAGAGTGGTGTATTTTCAGCACTACAGTGTACAGTCTTGTATTAAGTTTAAT 1649
Db 82 TTTTCAGAGAGTGGTGTATTTTCAGCACTACAGTGTACAGTCTTGTATTAAGTTTAAT 23
Qy 1650 AAAAGTACATGTTAACTTAA 1671
Db 22 AAAAGTACATGTTAACTTAA 1

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RESULT 4
 AI493618/c 657 bp mRNA EST 30-MAR-1999
 LOCUS t339e07.x1 NCI-CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2120676 3'
 DEFINITION similar to gb:L06797 PROBABLE G PROTEIN-COUPLED RECEPTOR ICR1
 HOMOLOG (HUMAN); mRNA sequence.
 ACCESSION AI493618
 NID 94394621
 VERSION AI493618.1 GI:4394621
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 657)
 AUTHOUS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT On May 18, 1998 this sequence version replaced gi:3137281.

Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Life Technologies catalog #: 11548-013
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/dbp/image/image.html

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    /issue_type="adenocarcinoma"
    /lab_host="DH10B"
    /note="Organ: pancreas; Vector: pCMV-Sport6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"
  BASE COUNT      232 a      130 c      109 g      184 t      2 others
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    Query Match      34.6%; Score 601.4; DB 47; Length 657;
    Best Local Similarity 98.2%; Pred. No. 8.6e-100;
    Matches 649; Conservative 0; Mismatches 8; Indels 4; Gaps 4;
    1017 TAAAACTCTGCGCCAGCAGCACTACCTCTGTGAGCAGAGGTCACCTCAAGATCCT 1076
    Db 657 TTAATAACTCTGCCAGCAGC-ACTCACCTCTGTGAGCAGAGGTCAGCCNCAAGAT-CT 600
    Qy 1077 CTCCAAAGGAAAGGAGGTGACATTCATCTGTTTCCACTAGTCTAGCTTCAAGTTT 1136
    Db 599 CTCCAAAGGAAAGGAGGTGAGCA-TCATCTGTTTCCACTAGTCTGAGTC-TCAAGTTT 542
    Qy 1137 TCATCCAGCTAACACAGATGAAAAGACTTTTATAGATTAATACCTTTTATTA 1196
    Db 541 TCATCCAGCTAACACAGATGAAAAGACTTTTATAGATTAATACCTTTTATTA 482
    Qy 1197 AGTTACACATTTTCAGATTAATAAAGACTGACCAATATTGACAGTTTATTTGCTGTT 1256
    Db 481 AGTTACACATTTTCAGATTAATAAAGACTGACCAATATTGACAGTTTATTTGCTGTT 422
    Qy 1257 GGATTTTGTCTGTGTTCTTTTATGTTTGTGAAGTTAATGACTTATTAATTAAT 1316
    Db 421 GGATTTTGTCTGTGTTCTTTTATGTTTGTGAAGTTAATGACTTATTAATTAAT 362
    Qy 1317 TTTTGTGTTTCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1376
    Db 361 TTTTGTGTTTCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 302
    Qy 1377 GTATGCTCTGTGTAGAGACTGTAGAAAAGGAGAACTGAACATTCAGAGCTGTAGTGAAT 1436
    Db 301 GTATGCTCTGTGTAGAGACTGTAGAAAAGGAGAACTGAACATTCAGAGCTGTAGTGAAT 242
    Qy 1437 CACGTAAAGCTAGAAATATATCCAGCTGTTTATGATAGTAAATCTCTCCATTCGCTG 1496
    Db 241 CACGTAAAGCTAGAAATATATCCAGCTGTTTATGATAGTAAATCTCTCCATTCGCTG 182
    Qy 1497 GAAGTTTTTCTGCTCTTAAGAGCTGATTTTGGCTGTAAGATGGCACTATAACCAA 1556
    Db 181 GAAGTTTTTCTGCTCTTAAGAGCTGATTTTGGCTGTAAGATGGCACTATAACCAA 122
    Qy 1557 GCCCAAGTGTATAGAAATCTGTTTTCAGTTTCAGAGTGTGTTGATTTTCAGCAC 1616
    Db 121 GCCCAAGTGTATAGAAATCTGTTTTCAGTTTCAGAGTGTGTTGATTTTCAGCAC 62
    Qy 1617 CTACAGTGTAGAGTCTGTATTAAGTTGTTAATAAAGTACATGTTAACTTAAAAAAA 1676
    Db 61 CTACAGTGTAGAGTCTGTATTAAGTTGTTAATAAAGTACATGTTAACTTAAAAAAA 2
    Qy 1677 A 1677
    Db 1 A 1

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726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Ronaldo.
BASE COUNT 220 a 116 c 89 g 164 t
ORIGIN

Query Match 33.9%; Score 589; DB 40; Length 589;
Best Local Similarity 100.0%; Pred. No. 1.5e-97;
Matches 589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1087 AAGCGAGTGCATTCATCTGTTCCACTGAGTGTGAGTCTCAAGTTTCACTCAGC 1146
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589 AAGCGAGTGCATTCATCTGTTCCACTGAGTGTGAGTCTCAAGTTTCACTCAGC 530
1147 TAACACAGATGTAAAGACTTTTATACGTAATAATACTTTTAAAGTACACAT 1206
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529 TAACACAGATGTAAAGACTTTTATACGTAATAATACTTTTAAAGTACACAT 470
1207 TTTTCAGATATAAAGACTGACCAATATTGTACAGTTTATGCTGTTGATTTTGT 1266
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469 TTTTCAGATATAAAGACTGACCAATATTGTACAGTTTATGCTGTTGATTTTGT 410
1267 CTGTGTTCTTATAGTTTGTGAGTTTAAATGACTTATTATTAATTTTGT 1326
|||||
409 CTGTGTTCTTATAGTTTGTGAGTTTAAATGACTTATTATTAATTTTGT 350
1327 TCATATGATGTGTGTAGTACAGAGCTGTGCGCAAGTTCTAGTGTATGTCG 1386
|||||
349 TCATATGATGTGTGTAGTACAGAGCTGTGCGCAAGTTCTAGTGTATGTCG 290
1387 TGTAGAGTGTAGAAAAAGGAGTGAACATTCAGAGCGGTGATGATACCTAAAGC 1446
|||||
289 TGTAGAGTGTAGAAAAAGGAGTGAACATTCAGAGCGGTGATGATACCTAAAGC 230
1447 TAGAATGATCCCGAGCTGTTATGATGATATCTCCATCCCGTGAAGTTT 1506
|||||
229 TAGAATGATCCCGAGCTGTTATGATGATATCTCCATCCCGTGAAGTTT 170
1507 CCTGTTCTTAAGAGTGTATTTGCTGAGAAAGTGGCACTTATAACCAAGCCCAAGTG 1566
|||||
169 CCTGTTCTTAAGAGTGTATTTGCTGAGAAAGTGGCACTTATAACCAAGCCCAAGTG 110
1567 GTATAGAAATCTGTTTTCAGTTTTCAGAGAGTGGTGAATTCAGACCTACAGTGA 1626
|||||
109 GTATAGAAATCTGTTTTCAGTTTTCAGAGAGTGGTGAATTCAGACCTACAGTGA 50
1627 CAGCTTGTATTAAGTGTATATAAAGTACATGTTAACTTAAAAA 1675
|||||
49 CAGCTTGTATTAAGTGTATATAAAGTACATGTTAACTTAAAAA 1
RESULT 7
AA411265 599 bp mRNA EST 17-MAY-1997
LOCUS zv24h06.r1 Soares NHMPL SI Homo sapiens cDNA clone IMAGE:754619 5'
DEFINITION similar to gb:L06797 PROBABLE G PROTEIN-COUPLED RECEPTOR LCR1
HOMOLOG (HUMAN); mRNA sequence.
ACCESSION AA411265
NID 92068847
VERSION AA411265.1 GI:2068847
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 599)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gelsel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
Moore, B., Schellenberg, K., Stephe, M., Tan, F., Theisling, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
TITLE Unpublished (1997)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1406946.

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 506.

FEATURES

SOURCE
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/clone="IMAGE:754619"
/clone_1b="Soares_NHMPL_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2BHM, pregnant uterus
NBHP, and fetal heart NBH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of 1 M.A.G.B. clones 260232-265223,
340488-345479, and 484488-489479."

BASE COUNT 168 a 93 c 117 g 221 t
ORIGIN
Query Match 32.7%; Score 567.8; DB 33; Length 599;
Best Local Similarity 98.6%; Pred. No. 1e-93;
Matches 583; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
1087 AAGCGAGTGCATTCATCTGTTCCACTGAGTGTGAGTCTCAAGTTTCACTCAGC 1146
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10 AAGCGAGTGCATTCATCTGTTCCACTGAGTGTGAGTCTCAAGTTTCACTCAGC 69
1147 TAACACAGATGTAAAGACTTTTATACGATTAATACTTTTAAAGTACACAT 1206
|||||
70 TAACACAGATGTAAAGACTTTTATACGATTAATACTTTTAAAGTACACAT 129
1207 TTTTCAGATATAAAGACTGACCAATATTGTACAGTTTATGCTGTTGATTTTGT 1266
|||||
130 TTTTCAGATATAAAGACTGACCAATATTGTACAGTTTATGCTGTTGATTTTGT 189
1267 CTGTGTTCTTATAGTTTGTGAGTTTAAATGACTTATTATTAATTTTGT 1326
|||||
130 CTGTGTTCTTATAGTTTGTGAGTTTAAATGACTTATTATTAATTTTGT 249
130 CTGTGTTCTTATAGTTTGTGAGTTTAAATGACTTATTATTAATTTTGT 249
1327 TCATATGATGTGTGTAGTACAGAGCTGTGCGCAAGTTCTAGTGTATGTCG 1386
|||||
250 TCATATGATGTGTGTAGTACAGAGCTGTGCGCAAGTTCTAGTGTATGTCG 309
1387 TGTAGAGTGTAGAAAAAGGAGTGAACATTCAGAGCGGTGATGATACCTAAAGC 1446
|||||
310 TGTAGAGTGTAGAAAAAGGAGTGAACATTCAGAGCGGTGATGATACCTAAAGC 369
1447 TAGAATGATCCCGAGCTGTTATGATGATATCTCCATCCCGTGAAGTTT 1506
|||||
370 TAGAATGATCCCGAGCTGTTATGATGATATCTCCATCCCGTGAAGTTT 429
1507 CCTGTTCTTAAGAGTGTATTTGCTGAGAAAGTGGCACTTATAACCAAGCCCAAGTG 1566
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1567 GTATAGAAATCTGTTTTCAGTTTTCAGAGAGTGGTGAATTCAGACCTACAGTGA 1626

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 /db_xref="taxon:9606"
 /clone="IMAGE:1272736"
 /clone_lib="NCI_CGAP_GCB1"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /note="Vector: p773D-Pac (Pharmacia) with a modified
 polylinker: Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20+, IgD-),
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
 primed with a Not I - oligo(dT) primer
 [5'-GTACCACTGCTGAGGAGGAGGCGGCGCTCATTTTCTTTTCTTTT-
 3']. Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified p773 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 205 a 105 c 81 g 165 t
 ORIGIN

Query Match 31.4%; Score 544.8; DB 38; Length 556;
 Best Local Similarity 98.7%; Pred. No. 1.5e-89;
 Matches 549; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1132 AGTTTCACCTCCAGTACACACAGATGTAAGACTTTTATACGATTAATACCTTT 1191
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 DB 556 AGTTTCACCTCCAGTACACACAGATGTAAGACTTTTATACGATTAATACCTTT 497
 OY 1132 TTTTAAGTACACATTTTTCAGATATAAAGACTGACCAATTTTACAGTTTATTCG 1251
 |||||||
 DB 496 TTTTAAGTACACATTTTTCAGATATAAAGACTGACCAATTTTACAGTTTATTCG 437
 OY 1252 TTGTTGATTTTGTCTGTGTTCTTTAGTTTGTGAAGTTTATGACTTATTATA 1311
 |||||||
 DB 436 TTGTTGATTTTGTCTGTGTTCTTTAGTTTGTGAAGTTTATGACTTATTATA 377
 OY 1312 TAAATTTTTTGTTCATATGATGTGTCTAGGACGACCTGTGGCCAAAGTCTTAG 1371
 |||||||
 DB 376 TAAATTTTTTGTTCATATGATGTGTCTAGGACGACCTGTGGCCAAAGTCTTAG 317
 OY 1372 TTGCTGTATGCTGTGAGAGAGCTGTGAAGGAAGGAACTGAACATTCAGAGCTGTAG 1431
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 DB 316 TTGCTGTATGCTGTGAGAGAGCTGTGAAGGAAGGAACTGAACATTCAGAGCTGTAG 257
 OY 1432 TGAATCAGTAAAGCTAGAAATGATCCCGAGCTTTATGATAGATATATCTTCATTC 1491
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 DB 256 TGAATCAGTAAAGCTAGAAATGATCCCGAGCTTTATGATAGATATATCTTCATTC 197
 OY 1492 CCGTGGAAAGCTTTTCCGTCTTTAAGACGTATTTTGTGTGAAGAGTGGCACTTATA 1551
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 DB 196 CCGTGGAAAGCTTTTCCGTCTTTAAGACGTATTTTGTGTGAAGAGTGGCACTTATA 137
 OY 1552 CCAAGGCCCAAGTGTATAGAAATGCTGTTTTCAGTTTCAGAGAGTGGTGTATTC 1611
 |||||||
 DB 136 CCAAGGCCCAAGTGTATAGAAATGCTGTTTTCAGTTTCAGAGAGTGGTGTATTC 77
 OY 1612 AGCACCCTAGTGTACAGTCTGTATTAAGTTGTAATTAAGATCATTTAAACTTAA 1671
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 DB 76 AGCACCCTAGTGTACAGTCTGTATTAAGTTGTAATTAAGATCATTTAAACTTAA 17
 OY 1672 AAAAAAAAAAAAAA 1687
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 DB 16 AAAAAAAAAAAAAA 1

RESULT 10
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 LOCUS AA610463
 DEFINITION np37b09.s1 NCI_CGAP.Lu1 Homo sapiens cDNA clone IMAGE:1142297 3'
 similar to gb:L06797 PROBABLE G PROTEIN-COUPLED RECEPTOR LCR1

ACCESSION AA610463
 NID 92458891
 VERSION AA610463.1 GI:2458891
 KEYWORDS EST.
 SOURCE
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia;
 TITLE Eutheria: Primates: Catarrhini: Hominiidae: Homo.
 JOURNAL NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Unpublished (1997)
 On Sep 12, 1996 this sequence version replaced gi:1395020.

Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Stratagene, Inc., David B. Krizman,
 Ph.D.
 CDNA Library Arraying: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdip/image/image.html

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 High quality sequence stop: 432.
 Location/Qualifiers
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 /clone_lib="NCI_CGAP.Lu1"
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 /lab_host="SOLR (kanamycin resistant)"
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 Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT.
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 3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3'
 Average insert size: 1.1 kb."

BASE COUNT 206 a 105 c 79 g 149 t
 ORIGIN

Query Match 31.0%; Score 539; DB 36; Length 539;
 Best Local Similarity 100.0%; Pred. No. 1.7e-88;
 Matches 539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1132 AGTTTCACCTCCAGTACACACAGATGTAAGACTTTTATACGATTAATACCTTT 1191
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 DB 539 AGTTTCACCTCCAGTACACACAGATGTAAGACTTTTATACGATTAATACCTTT 480
 OY 1192 TTTTAAGTACACATTTTTCAGATATAAAGACTGACCAATTTTACAGTTTATTCG 1251
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 DB 479 TTTTAAGTACACATTTTTCAGATATAAAGACTGACCAATTTTACAGTTTATTCG 420
 OY 1252 TTGTTGATTTTGTCTGTGTTCTTTAGTTTGTGAAGTTTATGACTTATTATA 1311
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 DB 419 TTGTTGATTTTGTCTGTGTTCTTTAGTTTGTGAAGTTTATGACTTATTATA 360
 OY 1312 TAAATTTTTTGTTCATATGATGTGTCTAGGACGACCTGTGGCCAAAGTCTTAG 1371
 |||||||
 DB 359 TAAATTTTTTGTTCATATGATGTGTCTAGGACGACCTGTGGCCAAAGTCTTAG 300
 OY 1372 TTGCTGTATGCTGTGAGAGAGCTGTGAAGGAAGGAACTGAACATTCAGAGCTGTAG 1431
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 DB 299 TTGCTGTATGCTGTGAGAGAGCTGTGAAGGAAGGAACTGAACATTCAGAGCTGTAG 240

Db 527 CTACACAGATGTAAGACT-TTTTATACGATTAATACTTTTTTAAGTACCA 469

QY 1206 TTTTCAGATATAAAGACTGACCAATATGTACAGTTTT -ATGCTGTGGATTT 1263

Db 468 TTTTTCAGATATAAAGACTGACCAATATGTACAGTTTTATGCTTGTGATTTT 409

QY 1264 TGGCTGTGTTCTTCTTGTGTTTGTGAGTTTATGACTATTTATATAATTTTTT 1323

Db 408 TGTCTGTGTTCTTCTTGTGTTTGTGAGTTTATGACTATTTATATAATTTTTT 349

QY 1324 GTTTCATATGATGTGTGTAGCAGACCTGTGGCAAGTTCTTGTGCTGTATGTC 1383

Db 348 GTTTCATATGATGTGTGTAGCAGACCTGTGGCAAGTTCTTGTGCTGTATGTC 289

QY 1384 TCGTGTAGGAGCTAGAAAAGGAGTGAACATTCAGAGCGTGTAGTGAATCAGTAA 1443

Db 288 TCGTGTAGGAGCTAGAAAAGGAGTGAACATTCAGAGCGTGTAGTGAATCAGTAA 229

QY 1444 AGCTAGAAATGATCCCGAGCTGTTATGATGATGAATCTCCATTCGCTGGAGCTT 1503

Db 228 AGCTAGAAATGATCCCGAGCTGTTATGATGATGAATCTCCATTCGCTGGAGCTT 169

QY 1504 TTTCTGTCTTAAAGAGTGTGTTGTGTAGAGATGGCACTTATAACCAAGCCCAA 1563

Db 168 TTTCTGTCTTAAAGAGTGTGTTGTGTAGAGATGGCACTTATAACCAAGCCCAA 109

QY 1564 GTGATATAGAAATCTGTGTTTTCAGTTTTCAGAGTGGTGTATTCAGACCTACAGT 1623

Db 108 GTGATATAGAAATCTGTGTTTTCAGTTTTCAGAGTGGTGTATTCAGACCTACAGT 49

QY 1624 GTACAGCTTGTATTAAGTGTATATAAAGTGAATGTTAACTTAA 1671

Db 48 GTACAGCTTGTATTAAGTGTATATAAAGTGAATGTTAACTTAA 1

RESULT 14
AA804282/c
LOCUS
DEFINITION
AA804282 536 bp mRNA EST 18-FEB-1998
n30h06.s1 NCI-GCAP_GCB0 Homo sapiens CDNA clone IMAGE:1242011 3'
similar to gb:L06797 PROBABLE G PROTEIN-COUPLED RECEPTOR LCR1
HOMOLOG (HUMAN);, mRNA sequence.

ACCESSION
NID
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AA804282
q2873569
AA804282.1 GI:2873569
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCI-GCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:1798484.

Contact: Robert Strausberg, Ph.D.
Tel.: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: Louis M. Staudt, M.D., Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILM at:
www-bio.llnl.gov/bdnp/image/image.html

Insert Length: 1513 Std Error: 0.00
Seq Primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 486.
Location/Qualifiers
1. 536

FEATURES
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/map="21"
/clone="IMAGE:1242011"
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/lab_host="SOLR (kanamycin resistant)"
/note="Organ: tonsil; Vector: Bluescript SK-; Site:1:
EcoRI; Site:2: XhoI; Cloned: 3rd; Directionally. Primer:
Oligo dt. Germinal center B-cells library constructed by
Dr. L. Staudt (NCI). 5' adaptor sequence: 5'
GAATTCGCCGACAG 3' 3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTT 3' Average insert size: 1.1 kb."

BASE COUNT 195 a 107 c 81 g 153 t

ORIGIN

Query Match 28.9%; Score 501.2; DB 38; Length 536;
Best Local Similarity 98.1%; Pred. No. 1.2e-81;
Matches 528; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

QY 1141 TCCAGCTAACACAGATGTAAAGACTTTTATACGATTAATACCTTTTTTAAGTT 1200

Db 536 TCCAGCTAACACAGATGTAAAGACTTTTATACGATTAATACCTTTTTTAAGTT 479

QY 1201 ACACATTTTCAGATATAAAGACTGACCAATATGTACAGTTTATGCTGTGGAT 1260

Db 478 ACACATTTTCAGATATAAAGACTGACCAATATGTACAGTTTATGCTGTGGAT 419

QY 1261 TTTTGTCTGTGTTCTTGTAGTTTGTGAAGTTAATGACTATTAATAATTTT 1320

Db 418 TTTTGTCTGTGTTCTTGTAGTTTGTGAAGTTAATGACTATTAATAATTTT 359

QY 1321 TTTTGTCTGTGTTCTTGTAGTTTGTGAAGTTAATGACTATTAATAATTTT 1380

Db 358 TTTTGTCTGTGTTCTTGTAGTTTGTGAAGTTAATGACTATTAATAATTTT 299

QY 1381 GTCCTGCTGTGAGCTGTAGAAAAGGAGTGAACATTCAGACGCTGTAGTGAATCAG 1440

Db 298 GTCCTGCTGTGAGCTGTAGAAAAGGAGTGAACATTCAGACGCTGTAGTGAATCAG 239

QY 1441 TAAAGCTAGAAATGATCCCGAGCTGTTATGATGATGAATCTCCATTCGCTGGAG 1500

Db 238 TAAAGCTAGAAATGATCCCGAGCTGTTATGATGATGAATCTCCATTCGCTGGAG 179

QY 1501 GTTTTCTGTCTTAAAGCTGATTTTGTGTGAAGAGTGCACCTATAACCAAGCCC 1560

Db 178 GTTTTCTGTCTTAAAGCTGATTTTGTGTGAAGAGTGCACCTATAACCAAGCCC 119

QY 1561 AAAGTGTATGAATGATGCTGTTTTCAGTTTTCAGAGTGGTGTGAATTCAGACCTAC 1620

Db 118 AAAGTGTATGAATGATGCTGTTTTCAGTTTTCAGAGTGGTGTGAATTCAGACCTAC 59

QY 1621 AGTGTACAGCTTGTATTAAGTGTATATAAAGTACATGTTAACTTAAAAA 1678

Db 58 AGTGTACAGCTTGTATTAAGTGTATATAAAGTACATGTTAACTTAAAAA 1

RESULT 15
AA426644/c
LOCUS
DEFINITION
AA426644 501 bp mRNA EST 16-OCT-1997
z447h11.s1 Soares ovary tumor NDHOT Homo sapiens CDNA clone
IMAGE:756837 3' similar to gb:L06797 PROBABLE G PROTEIN-COUPLED
RECEPTOR LCR1 HOMOLOG (HUMAN);, mRNA sequence.

ACCESSION
NID
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE

AA426644
q2107314
AA426644.1 GI:2107314
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 501)

